

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 01:44:06 ; Search time 2114 Seconds

(without alignments)
10333.841 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534
Sequence: 1 gtcccaatctgaagtgaag.....aaaaaaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 segs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBndl:.*
1: gb_ba:.*
2: gb_htg:.*
3: gb_in:.*
4: gb_om:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pl:.*
9: gb_pr:.*
10: gb_ro:.*
11: gb_sts:.*
12: gb_sy:.*
13: gb_un:.*
14: gb_vi:.*
15: em_ba:.*
16: em_fun:.*
17: em_hum:.*
18: em_in:.*
19: em_mu:.*
20: em_om:.*
21: em_or:.*
22: em_ov:.*
23: em_pat:.*
24: em_ph:.*
25: em_pl:.*
26: em_ro:.*
27: em_sts:.*
28: em_un:.*
29: em_vi:.*
30: em_htg_hum:.*
31: em_htg_inv:.*
32: em_htg_other:.*
33: em_htg_mus:.*
34: em_htg_pln:.*
35: em_htg_rtd:.*
36: em_htg_mam:.*
37: em_htg_vtc:.*
38: em_sy:.*
39: em_htgo_hum:.*
40: em_htgo_mus:.*
41: em_htgo_other:.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	518.4	97.1	530	9 AF096895	AF096895 Homo sapi
2	493.4	92.4	515	6 AR306550	AR306550 Sequence
3	493.4	92.4	515	6 AX061624	AX061624 Sequence
4	466.8	87.4	500	6 BD085905	BD085905 Elongatio
5	465.8	87.2	526	6 AR275027	AR275027 Sequence
6	411.4	77.0	413	6 BD085952	BD085952 Elongatio
7	405.4	75.9	415	6 BD023892	BD023892 Sequence
8	349.4	65.4	593	9 AF145216	AF145216 Homo sapi
9	349.4	65.4	593	9 AF145216	AF145216 Homo sapi
10	338	63.3	688	9 BC004380	BC004380 Homo sapi
11	325.4	60.9	655	9 AF057306	AF057306 Homo sapi
12	321.8	60.3	669	6 AR306591	AR306591 Sequence
13	321.8	60.3	669	6 AX061665	AX061665 Sequence
14	316.4	59.3	434	9 AF135381	AF135381 Homo sapi
15	278	52.1	485	11 G30204	G30204 human SRS
16	214.4	40.1	59554	6 AX695587	AX695587 Sequence
17	214.4	40.1	97075	6 AC010289	AC010289 Homo sapi
18	214.4	40.1	151620	2 AC018589	AC018589 Homo sapi
19	214.4	40.1	188460	9 AC010542	AC010542 Homo sapi
20	214	40.1	269	6 BD030595	BD030595 Sequence
21	210.2	39.4	321	6 BD139357	BD139357 Extended
22	205	38.4	207	6 AX330610	AX330610 Sequence
23	205	38.4	207	6 AX330787	AX330787 Sequence
24	205	38.4	207	6 AX331008	AX331008 Sequence
25	205	38.4	207	6 AX408097	AX408097 Sequence
26	185.2	34.7	495	6 AX079435	AX079435 Sequence
27	184.8	34.6	180702	9 AC018557	AC018557 Homo sapi
28	165.4	31.0	523	10 AF253064	AF253064 Rattus no
29	158.4	29.7	6283	6 AX252053	AX252053 Sequence
30	158.4	29.7	6283	6 AX344831	AX344831 Sequence
31	158.4	29.7	6283	6 AX348836	AX348836 Sequence
32	135	25.3	568	10 AY047360	AY047360 Mus muscu
33	126	23.6	682	10 AF253065	AF253065 Rattus no
34	119.4	22.4	6283	6 AX252052	AX252052 Sequence
35	119.4	22.4	6283	6 AX344830	AX344830 Sequence
36	119.4	22.4	6283	6 AX348835	AX348835 Sequence
37	78.4	14.7	45256	9 AC000090	AC000090 Homo sapi
38	73.4	13.7	137334	10 AC121952	AC121952 Mus muscu
39	73.4	13.7	171595	2 AC121275	AC121275 Mus muscu
40	73.4	13.7	209366	2 AC128918	AC128918 Rattus no
41	73.4	13.7	213593	2 AC131402	AC131402 Rattus no
42	73.4	13.7	273571	2 AC112851	AC112851 Rattus no
43	71.2	13.3	682	10 AF401531	AF401531 Mus muscu
44	70.2	13.1	189981	2 AC137048	AC137048 Rattus no
45	70.2	13.1	213593	2 AC131402	AC131402 Rattus no

ALIGNMENTS

RESULT 1
AF096895 530 bp mRNA linear PRI 18-JUL-2001
LOCUS DEFINITION Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.
ACCESSION AF096895
VERSION AF096895.2 GI:9989691
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 530)
Han,W., Lou,Y., Tang,J., Zhang,Y., Chen,Y., Li,Y., Gu,W., Huang,T.,
Gul,L., Tang,Y., Li,F., Song,Q., Di,C., Wang,L., Shi,Q., Sun,R.,
Xia,D., Rui,M., Tang,J. and Ma,D.

REFERENCE	TITLE
JOURNAL	Molecular cloning and characterization of chemokine-like factor 1 (CKLF1), a novel human cytokine with unique structure and potential chemotactic activity
MEDLINE	Biochem. J. 357 (Pt 1), 127-135 (2001)
PUBMED	21308461
REFERENCE	11415443
AUTHORS	2 (bases 1 to 530)
TITLE	Han, W. L., Li, Y., Zhang, Y. M., Di, C. H., Song, Q. S. and Ma, D. L.
JOURNAL	Direct Submission
REFERENCE	Submitted (03-Oct-1998) Immunology, Beijing Medical University, 38 Xue Yuan Rd., Beijing 100083, China
AUTHORS	3 (bases 1 to 530)
TITLE	Han, W. L.
REFERENCE	Direct Submission
AUTHORS	Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
REFERENCE	Sequence update by submitter
COMMENT	On Sep 7, 2000 this sequence version replaced gi:6288733.
FEATURES	Location/Qualifiers
source	1..530
	/organism="Homo sapiens"
	/mol_type="mRNA"
	/db_xref="taxon:9606"
	/cell_line="U937"
	/note="exposed to phytohaemagglutinin (PHA)"
gene	1..530
	/gene="CKLF1"
	/note="synonym: UCK-1"
	148..447
	/gene="CKLF1"
	/note="increased expression in PHA stimulated cells; expression inhibited by IL-10"
CDS	/codon_start=1
	/product="chemokine-like factor 1"
	/protein_id="AAF06722.1"
	/db_xref="GI:6288734"
	/translation="MDNVQPKIKRPFCSYKGVKMLRDIINSLVTVMILVSVLALIEETTLTVGGVGFALVTAVCCIALALLYRLFLNFPSPQKKPVEKKEVYL"
BASE COUNT	156 a 108 c 137 g 129 t
ORIGIN	
Query Match	97.1%; Score 518.4; DB 9; Length 530;
Best Local Similarity	99.8%; Pred. No. 5,5e-116;
Matches	519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy	15 GTGAAGCCGAGCTGGCGCAGAAAGTATGGGGAAGGCGGTCTCCGCGCGGTGGCTTCT 74
Db	11 GGAAGCCGAGCTGGCGCAGAAAGTATGGGGAAGGCGGTCTCCGCGCGGTGGCTTCT 70
Oy	75 ATCGCTTGCGAAGACTTACTCAGGACGACGCTGGAAGAGTGGAGAAAGTGCTGTG 134
Db	71 ATCGCTTGCGAAGACTTACTCAGGACGACGCTGGAAGAGTGGAGAAAGTGCTGTG 130
Oy	135 CTGGGCTGCGACGCGATGATAACGTGCAGCCGAAATATAAATCATGCGCCCTTTGCT 194
Db	131 CTGGGCTGCGACGCGATGATAACGTGCAGCCGAAATATAAATCATGCGCCCTTTGCT 190
Oy	195 TCAGTGTAAAGCCACGCTGAAGAGCTGCGCGCTGGATATATATCACTCATCTGGTAAC 254
Db	191 TCAGTGTAAAGCCACGCTGAAGAGCTGCGCGCTGGATATATATCACTCATCTGGTAAC 250
Oy	255 CAGTATTCATGCTCATCTATCTGTGTGGCACTGATACGAAACCAACATTTGACAG 314
Db	251 CAGTATTCATGCTCATCTATCTGTGTGGCACTGATACGAAACCAACATTTGACAG 310
Oy	315 TTGGTGAAGGGGTGTTTSCACTTGTGACAGCAGTATGCTGTCTTGGCGAGCGGGCCCTTA 374
Db	311 TTGGTGAAGGGGTGTTTSCACTTGTGACAGCAGTATGCTGTCTTGGCGAGCGGGCCCTTA 370
Oy	375 TTATACCGGAAGCTTCTGTTCATATCCCAACGGTCTTACCAAAAAAGCTGTGCATGAA 434
Db	371 TTATACCGGAAGCTTCTGTTCATATCCCAACGGTCTTACCAAAAAAGCTGTGCATGAA 430

OY		435	AAAAAGAACTTTGGTAATTTAATTATAACTTCTTTTGATTGTAACGAAGAATTAACAATATTT	494
Db		431	AAAAGAAAGTTTTGTAAATTTTAAATTAATTACTTTTGTAGTAGCACTAAGATTTAAACATATTT	490
OY		495	TCTGTATTCTTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	534
Db		491	TCTGTATTCTTCACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	530
 RESULT 2 AR306550 515 bp DNA linear PAT 12-JUN-2003				
LOCUS		AR306550		
DEFINITION		Sequence 29 from patent US 6548633.		
ACCESSION		AR306550		
VERSION		AR306550.1	GI:31696619	
KEYWORDS		.		
SOURCE		Unknown.		
ORGANISM		Unknown.		
REFERENCE		Unclassified.		
AUTHORS		1 (bases 1 to 515)		
TITLE		Edwards,J.,B.D.M., Bougueleret,L. and Jobert,S.		
JOURNAL		Complementary DNA's encoding proteins with signal peptides		
FEATURES		Patent: US 6548633-A 29 15-Apr-2003;		
		Location/Qualifiers		
	source	1..515		
		/organism="unknown"		
BASE COUNT		143 a 106 c 135 g 130 t	1 others	
ORIGIN				
Query Match		92.4%; Score 493.4; DB 6; Length 515;		
Best Local Similarity		99.4%; Pred. No. 7e-110;		
Matches		505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;		
OY		15	GTAAGACCAGACTGGCGCAGAAAGTAGAGGAGGCGGTGCCTCCGCCGCGTGGCGGTGGCT	74
Db		8	GGGAAGCCGACACTGGGCGCAGAAAGTAGGGAAGGCGGTGCTCCG-CGCGGTGGCNGTTGCT	66
OY		75	ATCGCTTGCAAACTTACTAGCAGCACCTGAGAAAGATTGAGGAAAGTGTCTGTG	134
Db		67	ATCGCTTGCAAACTTACTAGCAGCACCTGAGAAAGATTGAGGAAAGTGTCTGTG	126
OY		135	CTGGGCTCGCAGAGCGCATGTGTAACGTGCAGCCGGAATTAACATGGCCCCCTTCTGCT	194
Db		127	CTGGGCTCGCAGAGCGCATGTGTAACGTGCAGCCGGAATTAACATGGCCCCCTTCTGCT	186
OY		195	TCAGTGTAAAGGCCACGTGAAGATGCTGCCGCTGATATTATCACTCACTGTGAACA	254
Db		187	TCAGTGTAAAGGCCACGTGAAGATGCTGCCGCTGATATTATCACTCACTGTGAACA	246
OY		255	CAGTAATTCATGCTCATGCTATCTGTGTTGGCACTGATTCGAGAACCCAAACATTGAACG	314
Db		247	CAGTAATTCATGCTCATGCTATCTGTGTTGGCACTGATTCGAGAACCCAAACATTGAACG	306
OY		315	TTGGTGAAGGGGSGTTHGSCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCTTA	374
Db		307	TTGGTGAAGGGGSGTTHGSCACTTGTGACAGCAGTATGCTGTCTTGCCGACGGGGCCCTTA	366
OY		375	TTTACCGGAAAGCTTCTGTTCATCCACAGCGGTCCTTACCAAGAAAAAGCCTGTGCATGAA	434
Db		367	TTTACCGGAAAGCTTCTGTTCATCCACAGCGGTCCTTACCAAGAAAAAGCCTGTGCATGAA	426
OY		435	AAAAAGAAAGTTTGTAAATTTAATTATACTTTTATAGTTTGATACTAAGATTTAAACATATTT	494
Db		427	AAAAAGAAAGTTTGTAAATTTAATTATACTTTTATAGTTTGATACTAAGATTTAAACATATTT	486
OY		495	TCTGTATTCTTCACAAAAAAAAAAAAAAAAAAAAA	522
Db		487	TCTGTATTCTTCACAAAAAAAAAAAAAAAAAAAAA	514
 RESULT 3 AX061624 515 bp DNA linear PAT 24-JAN-2001				
LOCUS		AX061624		

Query Match	Best Local Similarity	87.4%; 97.8%;	Score 466.8; Pred. No. 2.2e-103;	DB 6;	Length 500;
Matches	488;	Conservative	4;	Mismatches 5;	Indels 2; Gaps 2
QY	23	GAGCTGGGCGAGAAATGAGGGGAGGGCGGCTCCGCCCGCGGTGGGG-TTGCTATCGCTT	:	:	:
DB	2	GAGCTGTNNCNSAATAGGGGAGGGCGGCTCCCGCMGAGTGGCGGDTGCTATCGCTT	:	:	:
QY	82	CGCAGAACCTCTCTCAGGAGCCAGGCTGAGAAAGTTGAGGGGAAAGTGCCTGCGGGTC	:	:	:
DB	62	CGCAGAACCTTACTTCAGGCGAGCCAGCTGAGAGAGTTGAGGGGAAAGTGCCTGCGGGTC	:	:	:
QY	142	TGCAGACCGAGTGTGATTAACGTGTCAGCCCGGAAATTAACAATCGCCCTTCTGCTTCAGTGT	:	:	:
DB	122	TGCAGACCGAGTGTGATTAACGTGTCAGCCCGGAAATTAACAATCGCCCTTCTGCTTCAGTGT	:	:	:
QY	202	GAAAGGCCACGCTGA-AGATGCTGGGGCTGGATATTAATCAACTCACTGCTGTAACAACAGTAT	:	:	:
DB	182	GAAAGGCCACGGAAGAATGCTCGCGCTGGATATTAATCAACTCACTGCTGTAACAACAGTAT	:	:	:
QY	261	TCATGCTCATGCTATCTGTGTGGTGGACGTGATCCAGAAACCAACAATGACAGTTGGTG	:	:	:
DB	242	TCATGCTCATGCTATCTGTGTGGTGGACGTGATCCAGAAACCAACAATGACAGTTGGTG	:	:	:

QY	321	GAGGGGTTTGGCACTTGTGAACAGAGATGCTGTGGCGACGGGGCCCTTATTAC	380
Db	302	GAGGGGTTTGGCACTTGTGAACAGAGATGCTGTGGCGACGGGGCCCTTATTAC	361
QY	381	GGAAGCTTCTGTCAATCCGACGGCTCTTACAGAAAAAGCCTGTGCATGAAAAAAG	440
Db	362	GGAAGCTTCTGTCAATCCGACGGCTCTTACAGAAAAAGCCTGTGCATGAAAAAAG	421
QY	441	AAAGTTTGTATTATTATTTACTTTTGTGATCTAAAGTATTAAACATATTTCTGT	500
Db	422	AAAGTTTGTATTATTATTTACTTTTGTGATCTAAAGTATTAAACATATTTCTGT	481
QY	501	TTCTTCCAAAAAAGAAAAA 519	
Db	482	TTCTTCCAAAAAAGAAAAA 500	
RESULT 5			
AR275027/c			
LOCUS	AR275027	526 bp	DNA linear PAT 10-APR-2007
DEFINITION	Sequence 164 from patent US 6506607.		
ACCESSION	AR275027		
VERSION	AR275027.1	GI:29707577	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 526)		
TITLE	Shyan,A.W.		
JOURNAL	Methods and compositions for the identification and assessment of		
FEATURES	prostate cancer therapies and the diagnosis of prostate cancer		
source	Patent: US 6506607-A 164 14-UN-2003;		
	Location/Qualifiers		
	1..526		
BASE COUNT	/organism="unknown"		
ORIGIN	133 a	136 c	113 g 143 t 1 others
Query Match	87.2%; Score 465.8; DB 6; Length 526;		
Best Local Similarity	99.0%; Pred.No. 3.9e-103;		
Matches	489; Conservative	0; Mismatches	3; Indels 2; Gaps 2
QY	28	GGGCGAAGTAAGGGGAGGGCGGTGCTCCGCCGCGTGGCGGTGCTATCGCTTGCAGA	87
Db	494	GGGCGAAGTAAGGGGAGGGCGGTGCTCCGCCGCGTGGCGGTGCTATCGCTTGCAGA	435
QY	88	ACCTACTAGGCAAGCAGACTGAGAAAGATTGAGGGAAAGTGCTGCTGGGCTGCAGA	147
Db	434	ACCTACTAGGCAAGCAGACTGAGAAAGATTGAGGGAAAGTGCTGCTGGGCTGCAGA	375
QY	148	CGCGATGATTAACGTGCAGACCGGAAATTAACATC-GCCCTTCTGCTTCAGTGTGAAG	206
Db	374	CGCGATGATTAACGTGCAGACCGGAAATTAACATCAGGCCCTTCTGCTTCAGTGTGAAG	315
QY	207	GCCACGTGAAGATGCTGCGGCTGATATTATCACTCACTGTGTAACAACAGTATTCATGC	266
Db	314	GCCACGTGAAGATGCTGCGGCTGATATTATCACTCACTGTGTAACAACAGTATTCATGC	255
QY	267	TCATCGTATCTGTGTGGCACTGTAATACAGAAACCAACAACTTGCACGTGGTGAAGGGG	326
Db	254	TCATCGTATCTGTGTGGCACTGTAATACAGAAACCAACAACTTGCACGTGGTGAAGGGG	195
QY	327	TGTTTGCACCTTGTGACACAGATGCTGCTTGCAGACGGGGCCCTTATTATTCACGGAAGC	386
Db	134	TGTTTGCACCTTGTGACACAGATGCTGCTTGCAGACGGGGCCCTTATTATTCACGGAAGC	135
QY	387	TTCTGTCAATCCGACGGCTCTTACAGAAAAAGCCTGTGCATGAAAAAAGAAAGTTT	446
Db	134	TTCTGTCAATCCGACGGCTCTTACAGAAAAAGCCTGTGCATGAAAAAAGAAAGTTT	75
QY	447	TGTATTTTATATTACTTTTATAGTTGATCTAAGTATTAAACATATTTTC-TGTATTTCTT	505
Db	74	TAAATTTTATATTACTTTTATAGTTGATCTAAGTATTAAACATATTTTCGTTATTTCTT	15

OY	506	CCAAAAA	519
Dd	14	CCAAAAA	1
RESULT 6			
BD085952			
LOCUS	BD085952	413 bp	DNA
DEFINITION	Elongation cDNA of secretory protein.		Linear
ACCESSION	BD085952		PAT 27-AUG-2002
VERSION	BD085952.1		
KEYWORDS	JF 2001523453-A/94.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 413)		
JOURNAL	Bouguieret, L., Ductert, A. and Edwards, J.B.D.M.		
	Elongation cDNA of secretory protein		
	Patent: JP 2001523453-A 94 27-NOV-2001;		
	GENSET		
COMMENT	OS Homo sapiens (human)		
	PN JP 2001523453-A/94		
	PD 27-NOV-2001		
	PF 13-NOV-1998 JP 2000521191		
	PR 13-NOV-1997 US 60/066677, 17-DEC-1997 US 60/069957 PR		
	09-FEB-1998 US 60/074121, 13-APR-1998 US 60/081563 PR		
	10-AUG-1998 US 60/096116, 04-SEP-1998 US 60/099273 PT LYDIE		
	BOUGUIERET, ALMERIC DUCLETT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS		
	PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC		
	C12N1/21,		
	PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC		
	Von Heijne matrix		
	CC score 4.09999990463257		
	CC seq VFMILIVSLALIP/ET		
	FH Key Location/Qualifiers		
	FT sig_peptide 46..189		
	FT polyA_signal 377..382		
	FT polyA_site 402..413.		
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	1..413		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
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ORIGIN			
Query Match	77.0%; Score 411.4; DB 6; Length 413;		
Best Local Similarity	99.8%; Pred. No. 7, 2e-90;		
Matches	412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
OY	107	TGAGAAAGTTGAAGGGAAGTGCTGTCTGGGTTCGCAGACGCATGATTAAGTGCAG	166
Dd	1	TGAGAAAGTTGAAGGGAAGTGCTGTCTGGGTTCGCAGACGCATGATTAAGTGCAG	60
OY	167	CCGAAAATAAACAATCGGCCCTTCTGCTCAAGTGAAGAAGCAGAGTGAAGATGCTGCAG	226
Dd	61	CCGAAAATAAACAATCGGCCCTTCTGCTCAAGTGAAGAAGCAGAGTGAAGATGCTGCAG	120
OY	227	CTGATATTATCAACTCACTGATTAACAAGATTAATCATGCTCATGATGATGCTGTGCA	286
Dd	121	CTGATATTATCAACTCACTGATTAACAAGATTAATCATGCTCATGATGATGCTGTGCA	180
OY	287	CTGATACCAGAAACCAACAATGACATTTGGTGAAGGGGCTTGGCACTTGTGACAGCA	346
Dd	181	CTGATACCAGAAACCAACAATGACATTTGGTGAAGGGGCTTGGCACTTGTGACAGCA	240
OY	347	GTATGCTCTCTGCGAGCGGGCCCTTAATTTTACCGAAGCTTCTGTCATCCACGCGT	406
Dd	241	GTATGCTCTCTGCGAGCGGGCCCTTAATTTTACCGAAGCTTCTGTCATCCACGCGT	300
OY	407	CCTTACCAAGAAAGCCTGTGCATGAAAAAAGATTGTGTAATTTAATTAATCTTT	466

Db	301	CGTTACCGAAGGAAAGGCTGTCATGAGAAAAAGAAAGTTTGTATATTTTATTTACTTTT	360
QY	467	TAGTTGATACCTAGATATTAACATATTTCTGATTTCTTCCAAAAA	519
Db	361	TAGTTGATACCTAGATATTAACATATTTCTGATTTCTTCCAAAAA	413
RESULT 7			
BD023892			
LOCUS			
DEFINITION	Sequence tag and encoded human protein.		
ACCESSION	BD023892		
VERSION	BD023892.1		
KEYWORDS	JP 2001269182-A/138.		
SOURCE	JP 2001269182-A/138.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 415)		
	Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.		
	Sequence tag and encoded human protein		
	Patent: JP 2001269182-A 138 02-OCT-2001;		
	GENSET		
COMMENT	OS Homo sapiens (human)		
	PN JP 2001269182-A/138		
	PD 02-OCT-2001		
	PF 24-FEB-2000 JP 2000118773		
	PR 26-FEB-1999 US 60/122487		
	PI JEAN BAPTISTE DUMAS MILNE EDWARDS,EIMERIC DUCCLAIR,JEAN YVES		
	PI JORDAN		
	PC C12N15/09,C07K14/435,C07K16/18,C12N1/15,C12N1/19,C12N1/21,PC		
	C12N5/10,		
	PC C12P21/02,C12P21/08,C1201/68//G06F17/30,C12N15/00,C12N5/00,PC		
	G06F15/40		
FEATURES			
source	1..415		
	/organism="Homo sapiens"		
	/mol_type="genomic DNA"		
	/db_xref="taxon:9606"		
BASE COUNT	101 a 97 c 126 g 91 t		
ORIGIN			
Query Match	75.9%; Score 405.4; DB 6; Length 415;		
Best Local Similarity	99.8%; Pred. No. 2.1e-89;		
Matches 406; Conservative	0; Mismatches 1; Indels 0; Gaps 0;		
QY	15	GTTGAAGCCGAGCTGGGGCGAAGTAAAGGAGGGCGGCTCCGCGGAGTGGGGTGGCT	74
Db	9	GGGAGGCGGAGCTGGGGCGAAGTAAAGGAGGGCGGCTCCGCGGAGTGGGGTGGCT	68
QY	75	ATCGCTTCGAGAACTCTACTCAGGCAAGCTGAGAAAGTTGAGGGAAGTGGCTGCTG	134
Db	69	ATCGCTTCGAGAACTCTACTCAGGCAAGCTGAGAAAGTTGAGGGAAGTGGCTGCTG	128
QY	135	CTGGGCTTCGAGAGCGCATGTATACGTGCAAGCCGAAATATTAACATCGCCCTTTCGT	194
Db	129	CTGGGCTTCGAGAGCGCATGTATACGTGCAAGCCGAAATATTAACATCGCCCTTTCGT	188
QY	195	TCAGTGTGAAGGCGCATGTGAAGTGTGGGGCTGATATTAATCACTCACTGGTAAACA	254
Db	189	TCAGTGTGAAGGCGCATGTGAAGTGTGGGGCTGATATTAATCACTCACTGGTAAACA	248
QY	255	CAGTATTCATGCTCATCGTATCTGTGTGTGGCACTGATACCAAGAAACCAACATTTGACAG	314
Db	249	CAGTATTCATGCTCATCGTATCTGTGTGTGGCACTGATACCAAGAAACCAACATTTGACAG	308
QY	315	TTCGTGAGAGGGGTTCGACCTTGTGACAGACAGATATCTGTCTTGGCCGAGGGGCCCTTA	374

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RESULT	8
AF15380	
LOCUS	689 bp mRNA linear PRI 07-SEP-2000
DEFINITION	Homo sapiens chemokine-like factor 2 (CXCLF2) mRNA, complete cds,
	alternatively spliced.
ACCESSION	AF15380
VERSION	AF15380.2 GI:989692
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL
1 (bases 1 to 689)	Han, W. L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.	Direct Submission	Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xueyuan Road, Beijing 100083, China	2 (bases 1 to 689)	Han, W. L.	Direct Submission	Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK	COMMENT	FEATURES	On Sep 7, 2000 this sequence version replaced gi:6630853.				
			location/Qualifiers				
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BASE COUNT
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QY	75	ATCGCTTCGCGAAGACTACTCAGCGACGACCTGAGAAAGTTGAGGAAAGTGTGCTG	134
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QY	135	CTGGGATCTGCAGACGCGGATGATACGTGCAGCGCGAAATATAAATCATGCGCCCTTCTGCT	194
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Qy	276	CTGTGTTGGACCTGATATCCAGAAACCAACAATTGACAGTTGTGTGAGGGGTGTTTGCAAC	335
Db	431	CTGTGTTGGACCTGATATCCAGAAACCAACAATTGACAGTTGTGTGAGGGGTGTTTGCCAC	490
Qy	336	TTGTGACAGCAGTATGCTGCTTGCCGAGCGGGGCCCTTATTTACCGAAGCTTGTTTCA	395
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RESULT 9	AF145216	593 bp	mRNA	linear	PRI 07-SEP-2000
LOCUS	AF145216				
DEFINITION	Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,				
ACCESSION	AF145216				
VERSION	AF145216.2				
KEYWORDS	GI:9989694				
SOURCE					
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo. 1 (bases 1 to 593) Han,W.L., Gu,W.F., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L. Direct Submission Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue Yuan Road, Beijing 100083, China 2 (bases 1 to 593) Han,W.L. Direct Submission Submitted (07-SEP-2000) Immunology, Peking University Health Science Center, Xueyuan Road 38, Beijing 100083, China Sequence update by submitter On Sep 7, 2000 this sequence version replaced gi:6625671. Location/Qualifiers 1..593 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /cell_line="U937" /note="from PHA stimulated cells" 1..593 /gene="CKLF4" /note="synonym: UCK" 148..510 /gene="CKLF4" /note="UCK-4; alternatively spliced"				
AUTHORS					
TITLE					
JOURNAL					
REMARK					
COMMENT					
FEATURES					
source					
gene					
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Best Local Similarity 79.8%; Pred. No. 1.3e-74;
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QY 135 CTGGGTCTGAGAGCGAGATGATAGCTGAGCCGAGAGAGAGAGAGAGAGAG 194
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REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Aarao, Ian Bosdet, Yaron Buterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywnski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeay, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeeadi, Jacqueline
Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
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Best Local Similarity 76.1%; Pred. No. 6.5e-72;
Matches 507; Conservative 0; Mismatches 0; Indels 159; Gaps 1;
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QY 148 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
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Qy 289 GATACCGAAGAACCAACATTTGACAGTGTGGAGGGGGTGGTTCACATTTGACAGAGT 348
Db 433 GATACCGAAGAACCAACATTTGACAGTGTGGAGGGGGTGGTTCACATTTGACAGAGT 492
Qy 349 ATGCTGCTTGGCCAGCGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCAGCGGTCC 408
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RESULT 11
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LOCUS Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.
DEFINITION AF057306
ACCESSION AF057306.1 GI:6648618
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 655)
AUTHORS Zhang, J. S., Nelson, M., Wang, L. and Smith D. I.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic and Foundation, Rochester, MN 55905, USA
Location/Qualifiers
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RESULT 12
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LOCUS AR306591
DEFINITION Sequence 70 from patent US 6548633.
ACCESSION AR306591
VERSION AR306591.1 GI:31696660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 669)
AUTHORS Edwards, J. B. D. M., Bougueleret, L. and Jobert, S.
TITLE Complementary DNA's encoding proteins with signal peptides
JOURNAL Patent: US 6548633-A 70 15-APR-2003;
Location/Qualifiers
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Best Local Similarity 75.6%; Pred. No. 5,9e-68;
Matches 504; Conservative 0; Mismatches 2; Indels 161; Gaps 2;

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LOCUS AX061665 669 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 70 from Patent WO0100806.
ACCESSION AX061665
VERSION AX061665.1 GI:12406789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS dumas mlne Edwards J.B., Bougueteloret L. and Jobert S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 70 04-JAN-2001;
GENSET (FR)
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Query Match 60.3%; Score 321.8; DB 6; Length 669;
Best Local Similarity 75.6%; Pred. No. 5.9e-68;
Matches 504; Conservative 0; Mismatches 2; Indels 161; Gaps 2;
QY 15 GTGAAGCCGAGCTGGGCGAGAAAGTAAGGAGGGGCTGCTCCGCGCGGTGGCT 74
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QY 456 ATATTACTTTTATGTTGATTAAGTATTAACATATTTCTGATTTCTCCAAAAAAA 515
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QY 516 AAAAAA 522
Db 663 AAAAAA 669

RESULT 14
LOCUS AF135381 434 bp mRNA linear PRI 07-SEP-2000
DEFINITION Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,
alternatively spliced.
ACCESSION AF135381
VERSION AF135381.2 GI:9989693
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 434)
AUTHORS Han W.L., Gu W., Li Y., Zhang Y., Song Q., Di C. and Ma D.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China

REFERENCE 2 (bases 1 to 434)
AUTHORS Han, W.L.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK Sequence update by submitter
COMMENT On Sep 7, 2000 this sequence version replaced gi:6630855.
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Best Local Similarity 81.3%; Pred. No. 1.1e-66;
Matches 423; Conservative 0; Mismatches 1; Indels 96; Gaps 1;
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QY 135 CTGGGCTCGAGAGCGGATGATTAACGTCGAGCCGAAATTAATCATGCGCCCTTCTGCT 194
DB 131 CTGGGCTCGAGAGCGGATGATTAACGTCGAGCCGAAATTAATCATGCGCCCTTCTGCT 190
QY 195 TCAGTGTGAAGGCGAGCTGAAGTCTGCGGCTGGAATATATCACTCACTGTGTAACA 254
DB 191 TCAGTGTGAAGGCGAGCTGAAGTCTGCGGCT----- 224
QY 255 CAGTATTCATGCTATGATCTGTGTGGACATGATACAGAAACCAACATTGACAG 314
DB 225 ----- 224
QY 315 TTGCTGAGGGGTGTTGCTGCTGTGACAGCAGATGCTGTCTTCCGAGCGGGCCCTTA 374
DB 225 -----GGTGTTCACCTTGTCAGCAGCATGATGCTGTCTTCCGAGCGGGCCCTTA 274
QY 375 TTACCCGAGAGCTTCTGTCATCCAGCGGCTCTTACCAAAAAAGCTGTGATGAAA 434
DB 275 TTACCCGAGAGCTTCTGTCATCCAGCGGCTCTTACCAAAAAAGCTGTGATGAAA 334
QY 435 AAAAAGAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 494
DB 335 AAAAAGAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 394
QY 495 TCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAAA 534
DB 395 TCTGTATTCTTCAAAAAAAAAAAAAAAAAAAAAA 434

RESULT 15
G30204/c G30204 485 bp DNA linear STS 05-OCT-1996
LOCUS

DEFINITION human STS SHGC-36487, sequence tagged site.
ACCESSION G30204
VERSION G30204.1 GI:1593755
KEYWORDS STS; STS sequence; primer; sequence tagged site.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 485)
AUTHORS Myers, R.M.
JOURNAL Unpublished (1996)
COMMENT
Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myers@shgc.stanford.edu
Primer A: ACTCTTTTTCATGCACAGC
Primer B: GCCCTATTACCGAGACT
STS size: 77
PCR Profile:
Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600
Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Taq Polymerase: 0.05 units/uL
Total Vol: 10 uL
Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3
Prepared with primer pairs provided by Sandoz, derived from T90569
-- Washington University/Merck EST sequence.
FEATURES
source
1. .485
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/map="16"
STS
primer_bind 69. .145
primer_bind 69. .91
complement (126. .145)
BASE COUNT 146 a 99 c 99 g 131 t 10 others
ORIGIN
Query Match 52.1%; Score 278; DB 11; Length 485;
Best Local Similarity 97.9%; Pred. No. 2.8e-57;
Matches 281; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 226 GCTGATATTATCACTCACTGTAACACAGTATTCATGCTATGCTATGCTGCTGCTG 285
DB 287 GCTGATATTATCACTCACTGTAACACAGTATTCATGCTATGCTATGCTGCTGCTG 228
QY 286 ACTGATACCAAGAACCAACATTCAGTGTGGAGGGGTGTTGCACTGTGACAGC 345
DB 227 ACTGATACCAAGAACCAACATTCAGTGTGGAGGGGTGTTGCACTGTGACAGC 168
QY 346 AGTATGCTGTCTTGGCGAGGGGCGCTTATTATTCACGGAACCTTCTGTTCAATCCACGG 405
DB 167 AGTATGCTGTCTTGGCGAGGGGCGCTTATTATTCACGGAACCTTCTGTTCAATCCACGG 108

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PT	disorders - has immunocyte chemotactic stimulating factor
XX	
PS	Example 4; Fig 1; 31bp; Chinese.
XX	
CC	This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis
CC	factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis
CC	activity and a haemopoiesis stimulating effect. The invention relates to
CC	UCK proteins, their encoding nucleotide sequences and antibodies and
CC	antagonists against the proteins. The nucleotide and protein sequences
CC	are useful for the preparation of a composition for the diagnosis and
CC	treatment of diseases associated with abnormal immunocyte function and
CC	low haemopoiesis function caused by radiotherapy and chemotherapy used to
CC	treat tumours and other diseases.
XX	
SQ	Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;
	Query Match 100.0%; Score 534; DB 21; Length 534;
	Best Local Similarity 100.0%; Pred. No. 2.3e-107;
	Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GTTCCCAATCTGAAGTGAAGCCGAGCTGGGCGAGAAAGTAGGGGAGGCGGTCTCCGCCG 60
DB	1 GTTCCCAATCTGAAGTGAAGCCGAGCTGGGCGAGAAAGTAGGGGAGGCGGTCTCCGCCG 60
QY	61 CGGTGGGCGGTTGCTATGCGTTGCGAAGACCTTACGAGCAGCAGCTGAGAGAGATTGAG 120
DB	61 CGGTGGGCGGTTGCTATGCGTTGCGAAGACCTTACGAGCAGCAGCTGAGAGAGATTGAG 120
QY	121 GGAAGTCTGCTGCTGGGTCTGCAGACCGCATGTGATACGTGCAGCCGAAATAAACA 180
DB	121 GGAAGTCTGCTGCTGGGTCTGCAGACCGCATGTGATACGTGCAGCCGAAATAAACA 180
QY	181 TCGCCCTTCTGCTTCACTGTGAAGGCCAGCTGAAGATGCTGCGCTGGATATTATCAA 240
DB	181 TCGCCCTTCTGCTTCACTGTGAAGGCCAGCTGAAGATGCTGCGCTGGATATTATCAA 240
QY	241 CTCACCTGTGAACAACAGTATTATCTCATCTATCTGTGTGGACATCATCGAAGAAC 300
DB	241 CTCACCTGTGAACAACAGTATTATCTCATCTATCTGTGTGGACATCATCGAAGAAC 300
QY	301 CACAACATTTGACAGTTGGTGAGGGGGTGTTCATCTTGTGACAGCAGTATGCTGCTTGC 360
DB	301 CACAACATTTGACAGTTGGTGAGGGGGTGTTCATCTTGTGACAGCAGTATGCTGCTTGC 360
QY	361 CGACGGGGCCCTTATTTACCGGAACCTTCTGTTCATCCGACGGGTCTTACCAAGAAAA 420
DB	361 CGACGGGGCCCTTATTTACCGGAACCTTCTGTTCATCCGACGGGTCTTACCAAGAAAA 420
QY	421 GCGTGTGATGAAAAAAGAGTTTGTATATTTATATTACTTTTGTAGTTGATATCTAA 480
DB	421 GCGTGTGATGAAAAAAGAGTTTGTATATTTATATTACTTTTGTAGTTGATATCTAA 480
QY	481 GTATTAAACATATTCTGTGATCTTCCAAAAAATTTTATTTTATTTTATTTTATTTT 534
DB	481 GTATTAAACATATTCTGTGATCTTCCAAAAAATTTTATTTTATTTTATTTTATTTT 534
RESULT 2	
AAAS44932	
ID	AAAS44932 standard; cDNA; 655 BP.
XX	
AC	AAAS44932;
XX	
DT	18-DEC-2001 (first entry)
DE	cDNA encoding novel human secretory protein, Seq ID No 13.
XX	
XX	Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
KM	ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
KM	transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
KM	amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
KM	ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
KM	gut protection; lung; liver fibrosis; immune deficiency; infection;

KW	severe combined immunodeficiency;SCID; autoimmune disorder; allergy;
KV	multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
KX	fertility; analgesic; pain; antigen; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200166689-A2.
XX	
PD	13-SEP-2001.
XX	
PE	05-MAR-2001; 2001WO-US04942.
XX	
PR	07-MAR-2000; 2000US-0519705.
PR	19-MAY-2000; 2000US-0574454.
PR	17-JUN-2000; 2000US-0596193.
PR	14-JUL-2000; 2000US-0616847.
PR	19-SEP-2000; 2000US-0665363.
PR	20-OCT-2000; 2000US-0693267.
XX	
PA	(HYSEQ-) HYSEQ INC.
XX	
PI	Tang YF, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
PI	Zhao QH, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
XX	
DR	WPI; 2001-589934/66.
DR	P-PSDB; AAU28032.
XX	
PT	Novel polypeptides and nucleic acids obtained from cDNA libraries
PT	prepared from various human tissues, for diagnosis and treatment of
PT	cancer, neurological, inflammatory, and autoimmune disorders -
XX	
PS	Claim 1; SEQ ID No 13; 107pp; English.

CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune response, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis,
 CC rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorythms or circadian cycles of rhythm,
 CC fertility, metabolism, catecholism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS4420-AAS5325 represent novel human secreted protein
 CC coding sequences of the invention.
 CC
 CC XX
 SQ Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;

Query Match	94.9%	Score 507	DB 22	Length 655
Best Local Similarity	100.0%	Prod. No. 1.9e-101		
Matches 507	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```
QY 19 AGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGCTGCTCCGCCGGGTGGCGGTGCTATCG 78
Db 1 AGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGCTGCTCCGCCGGGTGGCGGTGCTATCG 60
QY 79 CTTGCGAAGAACTTACTAGGCGAGCCAGCTGAGAAAGTTAGAGGAAAGTCTGCTGTGG 138
Db 61 CTTGCGAAGAACTTACTAGGCGAGCCAGCTGAGAAAGTTAGAGGAAAGTCTGCTGTGG 120
QY 139 GTCTGCGAGAGCGGATGATGATACGTGACGCGAAATATAAACATGCCCCCTTCTGCTTCA 198
Db 121 GTCTGCGAGAGCGGATGATGATACGTGACGCGCGAAATATAAACATGCCCCCTTCTGCTTCA 180
QY 199 TGTGAAGGCGCAGCTGAAGATGCTGCGGCTGATATTAATCACTACTGCTAAACAAGT 258
Db 181 TGTGAAGGCGCAGCTGAAGATGCTGCGGCTGATATTAATCACTACTGCTAAACAAGT 240
QY 259 ATTGATCTCATGCTATCTGTTGTCGATGATCCGAAACCAACATTTGACAGTTGG 318
Db 241 ATTGATCTCATGCTATCTGTTGTCGATGATCCGAAACCAACATTTGACAGTTGG 300
QY 319 TGGAGGGGTGTTGCACTTGTGACAGAGTATGCTGCTTCCGACGGGGCCCTTATTTA 378
Db 301 TGGAGGGGTGTTGCACTTGTGACAGAGTATGCTGCTTCCGACGGGGCCCTTATTTA 360
QY 379 CCGGAAAGCTTCTGTTCAATCCAGCGGTCCTTACAGAAAAAGCCTGTGATGAATAA 438
Db 361 CCGGAAAGCTTCTGTTCAATCCAGCGGTCCTTACAGAAAAAGCCTGTGATGAATAA 420
QY 439 AGAAGTTTGTATTTATTTATTTACTTTTGTGATGATGATTAATTAATTTCTG 498
Db 421 AGAAGTTTGTATTTATTTATTTACTTTTGTGATGATGATTAATTAATTTCTG 480
QY 499 TATTCTTCCAAAAAATTTTAAAAA 525
Db 481 TATTCTTCCAAAAAATTTTAAAAA 507

RESULT 3
AAH98515/c
ID AAH98515 standard; cDNA; 538 BP.
XX
AC AAH98515;
XX
DE 12-OCT-2001 (first entry)
XX
Human EST-derived coding sequence SEQ ID NO: 372.
XX
Human, sheep, pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dzmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
DR P-PSDB; AAM23856.
XX
```

```
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 451; 1275bp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

Query Match 93.3%; Score 498.2; DB 22; Length 538;
Best Local Similarity 99.4%; Pred. No. 1.5e-99;
Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 15 GTGAAGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTGCTCCGCCGGGTGGCGGTGCT 74
Db 503 GGAAGCCGAGCTGGGCGAGAAAGTAGAGGAGGCGGTGCTCCGCCGGGTGGCGGTGCT 444
QY 75 ATGCTTCCGAGAACTTACTAGGCGAGCCAGCTGAGAAAGATTGAGGAAAGTGTGCTG 134
Db 443 ATGCTTCCGAGAACTTACTAGGCGAGCCAGCTGAGAAAGATTGAGGAAAGTGTGCTG 384
QY 135 CTGGGCTGCGAGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 194
Db 383 CTGGGCTGCGAGACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 324
QY 195 TCAGTGAAAGGCGACGTAAGATGCTGCGGTGATATTAATCACTACTGATTAACA 254
Db 323 TCAGTGAAAGGCGACGTAAGATGCTGCGGTGATATTAATCACTACTGATTAACA 264
QY 255 CAGTATTCATGCTCATGCTATCTGCTGTGGCAGTATCCAGAAACCAACATTGACAG 314
Db 263 CAGTATTCATGCTCATGCTATCTGCTGTGGCAGTATCCAGAAACCAACATTGACAG 204
QY 315 TTGGTGGAGGGGTGTTGCACTTGTGACAGCAATATGCTCTTGGCCGAGGGGCCCTTA 374
Db 203 TTGGTGGAGGGGTGTTGCACTTGTGACAGCAATATGCTCTTGGCCGAGGGGCCCTTA 144
QY 375 TTTACCGGGAAGCTTCTGTTCAATCCAGCGGTCCTTACAGAAAAAGCCTGTGATGAA 434
Db 143 TTTACCGGGAAGCTTCTGTTCAATCCAGCGGTCCTTACAGAAAAAGCCTGTGATGAA 84
QY 435 AAAAAGAAAGTTTGTATTTATTTATTTACTTTTGTGATGATTAATTAATTAATTAAT 494
Db 83 AAAAAGAAAGTTTGTATTTATTTATTTACTTTTGTGATGATTAATTAATTAATTAAT 24
QY 495 TCTGTATTTCTTCAAAAAA 517
Db 23 TCTGTATTTCTTAAAAA 1

RESULT 4
AAH98548/c
ID AAH98548 standard; cDNA; 538 BP.
XX
AC AAH98548;
XX
DE 12-OCT-2001 (first entry)
XX
Human EST-derived coding sequence SEQ ID NO: 405.
XX
Human, sheep, pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
```

XX WO200154477-A2.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-US02687.
XX 25-JAN-2000; 2000US-0491404.
XX 17-JUL-2000; 2000US-0617746.
XX 03-AUG-2000; 2000US-0631451.
XX 15-SEP-2000; 2000US-0663870.
XX (HvSE-) HvSEQ INC.
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
XX Cao Y, Dermanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
XX P-PSDB; AAM23889.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX antibodies and research use -
XX Claim 1; Page 467; 1275bp; English.
XX The present invention provides the protein and coding sequences of novel
XX proteins from a variety of organisms, including human, dog, cat, horse,
XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX from the organism of interest. They can be used in diagnostics,
XX forensics, gene mapping, identification of mutations, to assess
XX biodiversity and for nutritional purposes. The present sequence is a cDNA
XX of the invention.
XX
XX Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;
SQ
Query Match 93.3%; Score 498.2; DB 22; Length 538;
Best Local Similarity 99.4%; Pred. No. 1.5e-99;
Matches 500; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 15 GTGAAGCCGAGCTGGGCGAGAAAGTGGGAGGCGGCTCCGCGCGTGGCGGCTTCT 74
DB 503 GGGAGCCGAGCTGGGCGAGAAAGTGGGAGGCGGCTCCGCGCGTGGCGGCTTCT 444
QY 75 ATCCGTTGCGAAGCTTCTCTAGGCGAGCGAGCTGAGAAAGTGGGAGGCGGCTGCTG 134
DB 443 ATCCGTTGCGAAGCTTCTCTAGGCGAGCGAGCTGAGAAAGTGGGAGGCGGCTGCTG 384
QY 135 CTGGGCTGCGAGCGCGATGATTAACGTGACCGGAAATTAACATGCGCCCTTCTGCT 194
DB 383 CTGGGCTGCGAGCGCGATGATTAACGTGACCGGAAATTAACATGCGCCCTTCTGCT 324
QY 195 TCAGTGTGAAGGCGCAGTGAAGTCTGGCGCTGGATTTATCACTCACTGTTGTAACA 254
DB 323 TCAGTGTGAAGGCGCAGTGAAGTCTGGCGCTGGATTTATCACTCACTGTTGTAACA 264
QY 255 CAGTATTCATGCTCATCTCTCTGTGTGGCAGTGAATCCAGAAACCAACATTTGACAG 314
DB 263 CAGTATTCATGCTCATCTCTGTGTGGCAGTGAATCCAGAAACCAACATTTGACAG 204
QY 315 TTGGTGAAGGGGTGTTTACCTGTGACAGAGTATGCTGCTTGCAGCGGGCCCTTA 374
DB 203 TTGGTGAAGGGGTGTTTACCTGTGACAGAGTATGCTGCTTGCAGCGGGCCCTTA 144
QY 375 TTTTACCGGAAGCTTGTGTTCAATCCAGCGGTCTTACCAAGAAAGCTGTGATGAAA 434
DB 143 TTTTACCGGAAGCTTGTGTTCAATCCAGCGGTCTTACCAAGAAAGCTGTGATGAAA 84
QY 435 AAAAAGAGTTTGTGATTTATATTAATTTATTTAGTTGATGATCAATGATTTAAATATT 494
DB 83 AAAAAGAGTTTGTGATTTATATTAATTTATTTAGTTGATGATCAATGATTTAAATATT 24
QY 495 TCTGTATTCTTCCAAAAAAA 517

DB 23 TCTGTATTCTTAAAAAAA 1
RESULT 5
ID AAH34835
ID AAH34835 standard; cDNA; 558 BP.
AC AAH34835;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.
XX
XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
XX WPI; 2001-235357/24.
DR P-PSDB; AAG75430.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers -
PT
XX Claim 1; Page 3428; 9803bp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77288 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patient's own production of P.
XX Additionally, N may be used to produce the colon cancer-associated P,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX present invention.
XX N.B. Pages 666 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;
Query Match 93.1%; Score 497.2; DB 22; Length 558;
Best Local Similarity 98.4%; Pred. No. 2.5e-99;
Matches 499; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 16 TGAAGCCGAGCTGGGCGAGAAAGTGGGAGGCGGCTCCGCGCGTGGCGGCTTCTA 75
DB 11 TGAAGTGGAGCTGGGCGAGAAAGTGGGAGGCGGCTCCGCGCGTGGCGGCTTCTA 70
QY 76 TCGGTTGGCAGAACTTACTAGCAGCAGCAGTGAAGAGTTGAGGAAAGTCTGCTGC 135
DB 71 TCGGTTGGCAGAACTTACTAGCAGCAGCAGTGAAGAGTTGAGGAAAGTCTGCTGC 130

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Qy 136 TGGGCTTCGACAGCCGATGATTAACGTGACCCGAAATAAATGATGCCCCCTTCTGCTT 195
Db 131 TGGGCTTCGACAGCCGATGATTAACGTGACCCGAAATAAATGATGCCCCCTTCTGCTT 190
Qy 196 CAGGTGTAAGGCGACCGTAAGATGCTGCGGCTGATTTTCAACTCATTGTAACAC 255
Db 191 CAGGTGTAAGGCGACCGTAAGATGCTGCGGCTGATTTTCAACTCATTGTAACAC 250
Qy 256 AGTATTCATGCTCATGCTATCTGTTGGCACTGATACCAAGAACCAACATTGACAGT 315
Db 251 AGTATTCATGCTCATGCTATCTGTTGGCACTGATACCAAGAACCAACATTGACAGT 310
Qy 316 TGGTGAAGGGGTGTTTGGCACTTGACAGCAGTATGCTGTTGCCGACGGGGCCCTTAT 375
Db 311 TGGTGAAGGGGTGTTTGGCACTTGACAGCAGTATGCTGTTGCCGACGGGGCCCTTAT 370
Qy 376 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTTGATGAAAA 435
Db 371 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTTGATGAAAA 430
Qy 436 AAAAGAAGTTTGTATTTTATTTATTTTACTTTTGTGATGATTAACATATTT 495
Db 431 AAAAGAAGTTTGTATTTTATTTTATTTTACTTTTGTGATGATTAACATATTT 490
Qy 496 CTGTATTTCTTCCAAAAAATTTTTTTTTT 522
Db 491 CTGTATTTCTTCCAAAAAATTTTTTTTTT 517
```

RESULT 6
ID AAA87730 standard; cDNA; 515 BP.

AC AAA87730;

DT 28-NOV-2000 (first entry)

DE Human secreted protein encoding cDNA SEQ ID #29.

XX Human; secreted protein; forensic procedure; gene therapy;
XX chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
XX cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
XX brain disorder; skeletal muscle disorder; obesity;
XX mitochondrial cytopathy; diabetes; atherosclerosis; Alzheimer's disease;
XX neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
XX septic shock; impotence; ss.

XX Homo sapiens.

OS W0200037491-A2.

PN 29-JUN-2000.

PD 20-DEC-1999; 99WO-1B02058.

PF 22-DEC-1998; 98US-0113686.

PR 25-JUN-1999; 99US-0141032.

XX (GEST) GENSET.

XX Bougueleret L, Dumas J, Duclert A;

XX WPI; 2000-442637/38.

XX P-PSDB; AAB25768.

XX Polynucleotides and polypeptides encoding proteins with signal
XX peptides, useful in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures -

XX Claim 1; Page 169-170; 306pp; English.

XX This sequence represents human cDNA encoding a secreted protein. The

CC invention relates to sequences AAA8725-A8774 which encode human
CC secreted proteins AAB25763-B25812. The proteins include signal peptides.
CC included in the invention are a host cell containing one of the cDNA
CC sequences, and a purified antibody capable of binding to one of the
CC secreted proteins. Also contained in the invention are methods for
CC storing the sequence data on a computer system, and a method for
CC identifying features of the cDNA sequences using a computer programme.
CC The cDNAs are useful for expressing secreted proteins or fragments to
CC obtain antibodies capable of specifically binding to the secreted
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
CC therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence.

CC Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

XX Query Match 92.4%; Score 493.4; DB 21; Length 515;
XX Best Local Similarity 99.4%; Pred. No. 1.7e-98;
XX Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 15 GTGAAGCCGAGCTGGGCGAGAGTAGGGGAGGGGGTCTCCGCGGCTGGCGGTGCT 74
Db 8 GGGAGCCGAGCTGGGCGAGAGTAGGGGAGGGGGTCTCCG CGGGTGGCGGTGCT 66

Qy 75 ATGCTTCGCAAGACCTTCTCAGGACCCAGCTGAGAAAGATTGAGGAAAGTCTCTG 134
Db 67 ATGCTTCGCAAGACCTTCTCAGGACCCAGCTGAGAAAGATTGAGGAAAGTCTCTG 126

Qy 135 CTGGGCTCGAGAGCGCATGATTAAGTGCAGCGGAATATAACATGCGCCCTTCTGCT 194
Db 127 CTGGGCTCGAGAGCGCATGATTAAGTGCAGCGGAATATAACATGCGCCCTTCTGCT 186

Qy 195 TCACTGTAAGAGCGCATGTAAGATGCTGGCGGTGATTTATCACTCACTGTGTAAC 254
Db 187 TCACTGTAAGAGCGCATGTAAGATGCTGGCGGTGATTTATCACTCACTGTGTAAC 246

Qy 255 CAGTATTCATGCTCATGCTATCTGTTGGCACTGATACCAAGAACCAACATTGACAG 314
Db 247 CAGTATTCATGCTCATGCTATCTGTTGGCACTGATACCAAGAACCAACATTGACAG 306

Qy 315 TTGGTGAAGGGGTGTTGCACTTGTAACAGATGCTGCTGGCAGGGGGCCCTTA 374
Db 307 TTGGTGAAGGGGTGTTGCACTTGTAACAGATGCTGCTGGCAGGGGGCCCTTA 366

Qy 375 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTTGATGAAAA 434
Db 367 TTACCGGAAGCTTCTGTTCAATCCGAGGCTCTTACCAAAAAAGCTTGATGAAAA 426

Qy 435 AAAAGAAGTTTGTATTTTATTTTATTTTACTTTTGTGATGATTAACATATTT 494
Db 427 AAAAGAAGTTTGTATTTTATTTTATTTTACTTTTGTGATGATTAACATATTT 486

Qy 495 TCTGTATTTCTTCCAAAAAATTTTTTTTTT 522
Db 487 TCTGTATTTCTTCCAAAAAATTTTTTTTTT 514

RESULT 7
ID AAF64012 standard; cDNA; 515 BP.

AC AAF64012;

DT 05-Apr-2001 (first entry)

DE cDNA encoding human secreted protein #13.

XX Secreted protein; prevention; treatment; diagnosis; disease;

KM infection; de.
 XX
 XX Homo sapiens.
 XX
 PN WC0200100806-A2.
 XX
 PD 04-JAN-2001.
 XX
 XX 21-JUN-2000; 2000WO-IB00951.
 XX
 XX 25-JUN-1999; 99US-0141032.
 PR 21-DEC-1999; 99US-0469099.
 XX
 XX (GEST) GENSET.
 XX
 PI Dumas Milne Edwards J, Bougueleret L, Jobert S;
 DR WPI; 2001-071487/08.
 XX
 PT 49 Secreted proteins and the nucleic acids encoding them, useful in
 PT gene therapy and for detecting similar sequences in samples -
 XX
 PS Claim 1; Page 225; 307pp; English.
 XX
 CC The present invention relates to 49 Secreted proteins and the cDNAs
 CC encoding them. The protein and nucleic acids may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate protein expression.
 XX
 SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;
 Query Match 92.4%; Score 493.4; DB 22; Length 515;
 Best Local Similarity 99.4%; Pred. No. 1.7e-98;
 Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 15 GTGAAGCCGAGCTGGGCGAGAGTGGAGGGGGGCTCCCGCGGCTGGCGTCT 74
 DB 8 GGGAGGCGGAGCTGGGCGAGAGTGGAGGGGGGCTCCG-CGGGCTGGCGTCT 66
 QY 75 ATGCGTTCGCGAAGCTACTCAGCAGCAGCAGCTGAGAGAGTTGAGGGAAAGTCTGCT 134
 DB 67 ATGCGTTCGCGAAGCTACTCAGCAGCAGCAGCTGAGAGAGTTGAGGGAAAGTCTGCT 126
 QY 135 CTGGGCTGCGAGAGCGATGATTAACGTGACGCCGAAATTAACATCGCCCTTCTGCT 194
 DB 127 CTGGGCTGCGAGAGCGATGATTAACGTGACGCCGAAATTAACATCGCCCTTCTGCT 186
 QY 195 TCAAGTGGAAAGGCGCAGTGAAGTCTGGCGCTGATATTATTAATCACTGCTTAACA 254
 DB 187 TCAAGTGGAAAGGCGCAGTGAAGTCTGGCGCTGATATTATTAATCACTGCTTAACA 246
 QY 255 CAGATTCATGCTCATGCTGATCTGTGGTGGCAGTATACCGAAGAACACAACTTGACAG 314
 DB 247 CAGATTCATGCTCATGCTGATCTGTGGTGGCAGTATACCGAAGAACACAACTTGACAG 306
 QY 315 TTGCTGAGAGGGGTGTTGCACTTGTCAGCAGAGTATCTGCTTCCGAGCGGGCCCTTA 374
 DB 307 TTGCTGAGAGGGGTGTTGCACTTGTCAGCAGAGTATCTGCTTCCGAGCGGGCCCTTA 366
 QY 375 TTTAACCGGAAGCTTCTGTTCAATCCAGCGGCTCTTAACGAAAGCCTGTGATGAAA 434
 DB 367 TTTAACCGGAAGCTTCTGTTCAATCCAGCGGCTCTTAACGAAAGCCTGTGATGAAA 426
 QY 435 AAAAAGAGTTTGTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTTTAA 494
 DB 427 AAAAAGAGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAA 486
 QY 495 TCTGTATTTCTCCAAAAAATTTTAAAAA 522
 DB 487 TCTGTATTTCTCCAAAAAATTTTAAAAA 514

AAV59598
 ID AAV59598 standard; DNA; 504 BP.
 XX
 AC AAV59598;
 XX
 DT 06-JAN-1999 (first entry)
 XX
 DE Human secreted protein gene 88 clone HAAVAV32.
 XX
 KM Human; secreted protein; fusion protein; gene therapy; protein therapy;
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
 KM developmental abnormality; foetal deficiency; blood; allergy; renal; de;
 KM immune system; ascuma; lymphocytic disease; brain; hepatic lymphoma;
 KM inflammation; ischaemic shock; Alzheimer's disease; osteoclast; thymus;
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
 XX
 OS Homo sapiens.
 XX
 PN WC09839448-A2.
 XX
 PD 11-SEP-1998.
 XX
 PF 06-MAR-1998; 98WO-US04493.
 XX
 PR 02-OCT-1997; 97US-0061060.
 PR 07-MAR-1997; 97US-0038621.
 PR 07-MAR-1997; 97US-0040161.
 PR 07-MAR-1997; 97US-0040162.
 PR 07-MAR-1997; 97US-0040163.
 PR 07-MAR-1997; 97US-0040333.
 PR 07-MAR-1997; 97US-0040334.
 PR 07-MAR-1997; 97US-0040336.
 PR 11-MAR-1997; 97US-0040626.
 PR 11-APR-1997; 97US-0043311.
 PR 11-APR-1997; 97US-0043312.
 PR 11-APR-1997; 97US-0043313.
 PR 11-APR-1997; 97US-0043314.
 PR 11-APR-1997; 97US-0043568.
 PR 11-APR-1997; 97US-0043569.
 PR 11-APR-1997; 97US-0043576.
 PR 11-APR-1997; 97US-0043578.
 PR 11-APR-1997; 97US-0043580.
 PR 11-APR-1997; 97US-0043669.
 PR 11-APR-1997; 97US-0043670.
 PR 11-APR-1997; 97US-0043671.
 PR 11-APR-1997; 97US-0043672.
 PR 11-APR-1997; 97US-0043674.
 PR 23-MAY-1997; 97US-0047492.
 PR 23-MAY-1997; 97US-0047500.
 PR 23-MAY-1997; 97US-0047501.
 PR 23-MAY-1997; 97US-0047502.
 PR 23-MAY-1997; 97US-0047503.
 PR 23-MAY-1997; 97US-0047581.
 PR 23-MAY-1997; 97US-0047582.
 PR 23-MAY-1997; 97US-0047583.
 PR 23-MAY-1997; 97US-0047584.
 PR 23-MAY-1997; 97US-0047585.
 PR 23-MAY-1997; 97US-0047586.
 PR 23-MAY-1997; 97US-0047587.
 PR 23-MAY-1997; 97US-0047588.
 PR 23-MAY-1997; 97US-0047589.
 PR 23-MAY-1997; 97US-0047590.
 PR 23-MAY-1997; 97US-0047592.
 PR 23-MAY-1997; 97US-0047593.
 PR 23-MAY-1997; 97US-0047594.
 PR 23-MAY-1997; 97US-0047595.
 PR 23-MAY-1997; 97US-0047596.
 PR 23-MAY-1997; 97US-0047597.
 PR 23-MAY-1997; 97US-0047598.
 PR 23-MAY-1997; 97US-0047599.
 PR 23-MAY-1997; 97US-0047600.

PR 23-MAY-1997; 97US-0047601.
 PR 23-MAY-1997; 97US-0047612.
 PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048974.
 PR 13-JUN-1997; 97US-0049610.
 PR 08-JUL-1997; 97US-0051926.
 PR 16-JUL-1997; 97US-0052874.
 PR 18-AUG-1997; 97US-0055724.
 PR 22-AUG-1997; 97US-0056630.
 PR 22-AUG-1997; 97US-0056631.
 PR 22-AUG-1997; 97US-0056632.
 PR 22-AUG-1997; 97US-0056636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057669.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 XX
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX
 XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
 PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS,
 PI K'aw H, Lafleur DM, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX
 XX WPI; 1998-506364/43.
 DR P-PSDB; AAW74818.
 XX
 XX New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 XX Claim 1; Page 320; 721pp; English.
 PS
 XX This sequence represents a nucleic acid molecule designated Gene 88 from
 CC the human cDNA clone HUAHV2 (deposited as clone ATCC 97901 and ATCC
 CC 209047) which encodes a secreted human protein. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human

CC immunoglobulin Pc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.
 CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological conditions
 CC can be diagnosed by determining the amount of the new polypeptides in a
 CC sample or by determining the presence of mutations in the new
 CC polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 XX
 XX Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;
 SQ
 Query Match 91.1%; Score 486.6; DB 19; Length 504;
 Best Local Similarity 99.0%; Pred. No. 5,1e-97;
 Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
 QY 21 CCGAGCTGGGCGAAGTAGGGAGGGGCGGTCTCCGCCGCGGTGGCTGTGCT 80
 DB 1 CCGAGCTGGGCGAAGTAGGGAGGGGCGGTCTCCGCCGCGGTGGCTGTGCT 59
 QY 81 TCGCAGAACTTACTCAGGCGACGCTGAGAAAGATTGAGGAAAGTCTGCTGGGT 140
 DB 60 TCGCAGAACTTACTCAGGCGACGCTGAGAAAGATTGAGGAAAGTCTGCTGGGT 119
 QY 141 CTCGACAGCGAGTAGTAACGTGACGCGCAAAATAAATCATGCCCTTCTGCTCAGTG 200
 DB 120 CTCGACAGCGAGTAGTAACGTGACGCGCAAAATAAATCATGCCCTTCTGCTCAGTG 179
 QY 201 TGAAGGCCACGTGAAGATGCTCGCGGTGATTTATCAACTGCTGTTAACAACAGTAT 260
 DB 180 TGAAGGCCACGTGAAGATGCTCGCGGTGATTTATCAACTGCTGTTAACAACAGTAT 239
 QY 261 TCATGCTCATCTGATCTGTTGGCACTGATACCAAAACACAACTTACAGCTTGGTG 320
 DB 240 TCATGCTCATCTGATCTGTTGGCACTGATACCAAAACACAACTTACAGCTTGGTG 299
 QY 321 GAGGGGTTGTGACCTTGACAGCAGATAGCTGCTGCGGCGGAGGCGCTTATTTAC 380
 DB 300 GAGGGGTTGTGACCTTGACAGCAGATAGCTGCTGCGGCGGAGGCGCTTATTTAC 359
 QY 381 GGAAGCTTCTGTTCAATCCAGCGGTCTTACCAAGAAAAGCCTGTGCATGAAAAAAG 440
 DB 360 GGAAGCTTCTGTTCAATCCAGCGGTCTTACCAAGAAAAGCCTGTGCATGAAAAAAG 419
 QY 441 AAGTTTGTATTTATTTATTTATTTAGTTTATTTATTTATTTATTTATTTATTTATTT 500
 DB 420 AAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 479
 QY 501 TTCTTCCAAAAAATAAAAAA 525
 DB 480 TTCTTCCAAAAAATAAAAAA 504
 XX
 XX RESULT 9
 XX AAS73585
 XX ID AAS73585 standard; cDNA; 504 BP.
 XX
 XX AAS73585;
 XX
 XX 15-JAN-2003 (first entry)
 XX
 XX Human cDNA #1 for novel secreted protein gene 88.
 DE Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
 KW Human; ss; gene; secreted protein; autoimmune disease; chemotaxis;
 KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
 KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
 KW cerebrovascular disorder; cerebral ischaemia; angiodysplasia; sunburn;
 KW nervous system disorders; Alzheimer's disease; infection;
 KW ocular disorder; corneal infection; wound healing; tissue regeneration;
 KW epithelial cell proliferation; organ transplantation; food additive;
 KW preservative; nutritional.

CC		22-AUG-1997;	97US-056632P.
PR		22-AUG-1997;	97US-056636P.
PR		22-AUG-1997;	97US-056637P.
PR		22-AUG-1997;	97US-056682P.
PR		22-AUG-1997;	97US-056684P.
PR		22-AUG-1997;	97US-056845P.
PR		22-AUG-1997;	97US-056862P.
PR		22-AUG-1997;	97US-056864P.
PR		22-AUG-1997;	97US-056872P.
PR		22-AUG-1997;	97US-056874P.
PR		22-AUG-1997;	97US-056875P.
PR		22-AUG-1997;	97US-056876P.
PR		22-AUG-1997;	97US-056877P.
PR		22-AUG-1997;	97US-056878P.
PR		22-AUG-1997;	97US-056879P.
PR		22-AUG-1997;	97US-056880P.
PR		22-AUG-1997;	97US-056881P.
PR		22-AUG-1997;	97US-056882P.
PR		22-AUG-1997;	97US-056884P.
PR		22-AUG-1997;	97US-056885P.
PR		22-AUG-1997;	97US-056887P.
PR		22-AUG-1997;	97US-056888P.
PR		22-AUG-1997;	97US-056890P.
PR		22-AUG-1997;	97US-056909P.
PR		22-AUG-1997;	97US-056910P.
PR		22-AUG-1997;	97US-056911P.
PR		22-AUG-1997;	97US-057761P.
PR		05-SEP-1997;	97US-057650P.
PR		05-SEP-1997;	97US-057669P.
PR		12-SEP-1997;	97US-058785P.
PR		12-OCT-1997;	97US-061060P.
R		06-MAR-1998;	98WC-US04493.
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA			
XX	Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR,		
P1	Andress GA, Yu G, Ni J, Peng P, Young PE, Greene JM, Ferrie AM;		
P1	Duan R, Hu J, Florence KA, Olsen HS, Edner R, Brewer LA;		
P1	Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;		
XX			
DR	WPI; 2002-634796/68.		
DR	P-PSDB; ABG95267.		
XX			
PT	New isolated human secreted protein for diagnosing, preventing,		
PT	treating or ameliorating medical conditions and used as a food additive		
PT	or preservative -		
PS	Example 1; SEQ ID No 98; 129pp; English.		
XX			
CC	The invention relates to an isolated protein that is one of 186 human		
CC	secreted proteins, given in the specification, encoded by one of		
CC	309 cDNA sequences also given in the specification. The protein is used		
CC	in a pharmaceutical composition used to prevent, treat or ameliorate a		
CC	medical condition in e.g. humans, mice, rabbits, goats, horses, cats,		
CC	dogs, chickens or sheep. Disorders which are diagnosed or treated include		
CC	autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative		
CC	disorders e.g. neoplasms of the breast or liver, cardiovascular disorders		
CC	e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,		
CC	angiogenesis, nervous system disorders e.g. Alzheimer's disease,		
CC	infections caused by bacteria, viruses and fungi and ocular disorders		
CC	e.g. corneal infection. The polypeptides can also be used to aid wound		
CC	healing and epithelial cell proliferation, to prevent skin aging due to		
CC	sunburn, to maintain organs before transplantation, for supporting cell		
CC	culture of primary tissues, to regenerate tissues and in chemotaxis. The		
CC	polypeptides can also be used as a food additive or preservative to		
CC	increase or decrease storage capabilities, fat content, lipid, protein,		
CC	carbohydrate, vitamins, minerals, cofactors and other nutritional		
CC	compounds. The present sequence represents a cDNA derived from a		

CC gene encoding one of the novel human secreted proteins of the invention.
CC Note: This sequence did not form part of the printed specification,
CC but was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=6420526B1.

XX Sequence 504 BP, 143 A, 106 C, 128 G, 127 T; 0 other;

Query Match 91.1%; Score 486.6; DB 24; Length 504;
Best Local Similarity 99.0%; Pred. No. 5.1e-97;
Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

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QY 21 CCGAGCTGGGGGAGAGTAGGGGGGGGCTCCCGCGGGGGGGGCTGCTAGTCT 80
D 1 CCGAGCTGGGGGAGAGTAGGGGGGGGCTCCCGCGGGGGGGGCTGCTAGTCT 59
QY 81 TCGAGAACCTACTCAGGAGCAGCAGTGAAGAGTTGAGGGAAAGTCTGCTGGGT 140
D 60 TCGAGAACCTACTCAGGAGCAGCAGTGAAGAGTTGAGGGAAAGTCTGCTGGGT 119
QY 141 CTGAGACGGGATGATTAACCTGAGCGGAAATAAACATCGCCCTTCTGCTTCA 200
D 120 CTGAGACGGGATGATTAACCTGAGCGGAAATAAACATCGCCCTTCTGCTTCA 179
QY 201 TGAAGGCGACGTAAGATGCTGCGCTGATATTATCACTGCTGTAACAAGTAT 260
D 180 TGAAGGCGACGTAAGATGCTGCGCTGATATTATCACTGCTGTAACAAGTAT 239
QY 261 TCATGCTCATGTAATCTGTTGGCTGATACGATACCAACAACATGACATGGTG 320
D 240 TCATGCTCATGTAATCTGTTGGCTGATACGATACCAACAACATGACATGGTG 299
QY 321 GAGGGGTGTTGCACTTGACAGCAGATGCTGCTTGCAGAGGGGCTTATTTACC 380
D 300 GAGGGGTGTTGCACTTGACAGCAGATGCTGCTTGCAGAGGGGCTTATTTACC 359
QY 381 GGAAGCTTGTTCATCCAGCGGCTCTTACCAAAAAAGCTGTGCAAAAAAAG 440
D 360 GGAAGCTTGTTCATCCAGCGGCTCTTACCAAAAAAGCTGTGCAAAAAAAG 419
QY 441 AAGTTTGTATTTTATTTATCTTTTATGTTGATTAATTAATTAATTTCTGTA 500
D 420 AAGTTTGTATTTTATTTATCTTTTATGTTGATTAATTAATTAATTTCTGTA 479
QY 501 TTCTTCCAAAAAATTTTTTTTTTTT 525
D 480 TTCTTCCAAAAAATTTTTTTTTTTT 504

RESULT 10
AAVS9746
ID AAVS9746 standard; DNA; 506 BP.
XX
AC AAVS9746;
XX
DT 19-JAN-1999 (first entry)
XX
DE Human secreted protein gene 88 clone HAAV12.
XX
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
XX diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
XX developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
XX immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
XX inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
XX cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
XX osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
XX endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN M09839448-A2.
XX
PD 11-SEP-1998.
XX
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PF 06-MAR-1998; 98MO-US04493.
XX
XX 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
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PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
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PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
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PR 11-APR-1997; 97US-043576P.
 PR 11-APR-1997; 97US-043578B.
 PR 11-APR-1997; 97US-043580P.
 PR 11-APR-1997; 97US-043669P.
 PR 11-APR-1997; 97US-043670P.
 PR 11-APR-1997; 97US-043671P.
 PR 11-APR-1997; 97US-043672P.
 PR 23-MAY-1997; 97US-047492P.
 PR 23-MAY-1997; 97US-047500P.
 PR 23-MAY-1997; 97US-047501P.
 PR 23-MAY-1997; 97US-047502P.
 PR 23-MAY-1997; 97US-047503P.
 PR 23-MAY-1997; 97US-047581P.
 PR 23-MAY-1997; 97US-047582P.
 PR 23-MAY-1997; 97US-047583P.
 PR 23-MAY-1997; 97US-047584P.
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 PR 23-MAY-1997; 97US-047586P.
 PR 23-MAY-1997; 97US-047587P.
 PR 23-MAY-1997; 97US-047589P.
 PR 23-MAY-1997; 97US-047590P.
 PR 23-MAY-1997; 97US-047592P.
 PR 23-MAY-1997; 97US-047593P.
 PR 23-MAY-1997; 97US-047594P.
 PR 23-MAY-1997; 97US-047595P.
 PR 23-MAY-1997; 97US-047596P.
 PR 23-MAY-1997; 97US-047597P.
 PR 23-MAY-1997; 97US-047598P.
 PR 23-MAY-1997; 97US-047599P.
 PR 23-MAY-1997; 97US-047600P.
 PR 23-MAY-1997; 97US-047601P.
 PR 23-MAY-1997; 97US-047612P.
 PR 23-MAY-1997; 97US-047613P.
 PR 23-MAY-1997; 97US-047614P.
 PR 23-MAY-1997; 97US-047615P.
 PR 23-MAY-1997; 97US-047617P.
 PR 23-MAY-1997; 97US-047618P.
 PR 23-MAY-1997; 97US-047632P.
 PR 23-MAY-1997; 97US-047633P.
 PR 06-JUN-1997; 97US-048964P.
 PR 06-JUN-1997; 97US-048974P.
 PR 13-JUN-1997; 97US-049610P.
 PR 08-JUL-1997; 97US-051926P.
 PR 16-JUL-1997; 97US-052874P.
 PR 18-AUG-1997; 97US-055724P.
 PR 22-AUG-1997; 97US-056630P.
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 PR 22-AUG-1997; 97US-056662P.
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 PR 22-AUG-1997; 97US-056881P.
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 PR 22-AUG-1997; 97US-056887P.
 PR 22-AUG-1997; 97US-056888P.
 PR 22-AUG-1997; 97US-056889P.
 PR 22-AUG-1997; 97US-056892P.

PR 22-AUG-1997; 97US-056893P.
 PR 22-AUG-1997; 97US-056894P.
 PR 22-AUG-1997; 97US-056903P.
 PR 22-AUG-1997; 97US-056908P.
 PR 22-AUG-1997; 97US-056909P.
 PR 22-AUG-1997; 97US-056910P.
 PR 22-AUG-1997; 97US-056911P.
 PR 22-AUG-1997; 97US-05761P.
 PR 05-SEP-1997; 97US-057650P.
 PR 05-SEP-1997; 97US-057669P.
 PR 12-SEP-1997; 97US-058785P.
 PR 02-OCT-1997; 97US-061060P.
 PR 06-MAR-1998; 98WO-US04493.
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX
 PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
 PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;
 PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX
 DR WPI: 2002-634796/68.
 DR P-PSDB; ABG95421.
 XX
 PT New isolated human secreted protein for diagnosing, preventing,
 PT treating or ameliorating medical conditions and used as a food additive
 PT or preservative
 PT
 XX
 XX Example 1; SEQ ID No 252; 129pp; English.
 XX
 CC The invention relates to an isolated protein that is one of 186 human
 CC secreted proteins, given in the specification, encoded by one of
 CC 309 cDNA sequences also given in the specification. The protein is used
 CC in a pharmaceutical composition used to prevent, treat or ameliorate a
 CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
 CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. The present sequence represents a cDNA derived from a
 CC gene encoding one of the novel human secreted proteins of the invention.
 CC Note: This sequence did not form part of the printed specification,
 CC but was obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docid=642052651.
 CC
 XX
 SQ Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;
 QY
 QY Query Match 89.6%; Score 478.6; DB 24; Length 506;
 QY Best Local Similarity 97.4%; Pred. No. 2.8e-95;
 QY Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 Db
 Db 37 GTAGGGAGGCGGCTGCTCCGCGCGGTGCGGTGCTATCGCTTCAGAACTTACTCA 96
 Db 2 GCAGGATTTGGCCAGGACCCCGCGGTGCGGTGCTATCGCTTCAGAACTTACTCA 61
 QY
 QY 97 GGCAGCAGCTGAGAGAGTTGAGGGAAGTCTGCTGCTGCGGTCTGCAACGCGATGGA 156
 Db 62 GGCAGCAGCTGAGAGAGTTGAGGGAAGTCTGCTGCTGCGGTCTGCAACGCGATGGA 121
 QY
 QY 157 TTAAGTCAGCCGCAAAATTAACAATGCGCCCTTCTGTTAGTGTGAAGCCACGCGTAA 216
 Db 122 TTAAGTCAGCCGCAAAATTAACAATGCGCCCTTCTGTTAGTGTGAAGCCACGCGTAA 181
 QY
 QY 217 GATGCTCGGCGGTGATTTATCACTGTAACAACAGTATTCATGCTCATCGTATC 276

```

Db      182 GATGCTGGCGCTGATATTAATCACTCACTGGTAACACAGTATTCATGCTCATCGATAC
Qy      277 TGTGTTGGCACTGATACAGAGAAACCAACAATGACAGTGGTGGAGGGGTTTGCACT
Db      242 TGTGTTGGCACTGATACAGAGAAACCAACAATGACAGTGGTGGAGGGGTTTGCACT
Qy      337 TGTGACAGCAGTATGCTGCTTGTGCGAGCGGGGCCCTTATTTACGGAAGCTTCTGTCA
Db      302 TGTGACAGCAGTATGCTGCTTGTGCGAGCGGGGCCCTTATTTACGGAAGCTTCTGTCA
Qy      397 TCCAGCGGCTCTTAACAGAAAGCCTGCGATGAAAGAAAGAGTTTGAATTTA
Db      362 TCCAGCGGCTCTTAACAGAAAGCCTGCGATGAAAGAAAGAGTTTGAATTTA
Qy      457 TATTAATCTTTAGTTGATTAAGTATTAACATTTCTGTAATCTTCCAAAAAAA
Db      422 TATTAATCTTTAGTTGATTAAGTATTAACATTTCTGTAATCTTCCAAAAAAA
Qy      517 AAAAAAAAAAAAAAAAAA 533
Db      482 AAAAAAAAAAAAAAAAAA 498

```

RESULT 12
AAx97826
ID AAX97826 standard; cDNA; 500 BP.

AAx97826;
DT 23-SEP-1999 (first entry)

DE Human secreted protein encoding cDNA #14.

KM Secreted protein; human; cytosolic; chromobiotic; osteopathic; forensic;
diagnostic; gene therapy; chromosome mapping; secretion vector; ss.

OS Homo sapiens.

XX WO9925825-A2.

XX 27-MAY-1999.

PF 13-NOV-1998; 98WO-1B01862.

PR 04-SEP-1998; 98US-0099272.

PR 13-NOV-1997; 97US-0066677.

PR 17-DEC-1997; 97US-0069957.

PR 09-FEB-1998; 98US-0074121.

PR 13-APR-1998; 98US-0081563.

PR 10-AUG-1998; 98US-0096116.

PA (GBST) GENSET.

PI Bouguetier L, Duclert A, Dumas Milne Edwards J;

DR WPI, 1999-347472/29.

PT P-PSDB; AAY36142.

XX Extended cDNAs encoding secreted proteins

XX Example 26; Page 173-174; 307pp; English.

CC AAX97813-X97906 represent extended cDNA's which encode novel human
CC secreted proteins (see AAY36129-Y36222) and which have cytosolic,
CC chromobiotic and osteopathic activity. The extended cDNAs can be used to
CC express secreted proteins or parts of them or to obtain antibodies
CC capable of binding to the secreted proteins. They may also be used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC Uses also include design of expression vectors and secretion vectors.

Query Match 87.4%; Score 466.8; DB 20; Length 500;
Best Local Similarity 97.8%; Pred. No. 1.1e-92;
Matches 488; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

```

Qy      23 GAGTGGCGCAGAAAGTAAAGGAGAGGGGCTGCTCCGCGGCTGGCGG-TTGCTATGGCTT
Db      2 GAGTGTNNCNNSAAGTAAAGGAGAGGGGCTGCTCCGCGGCTGGCGG-TCGCTATGGCTT
Qy      82 CGCAGAACTACTACAGCAGCCAGCTGAGAAAGTTGAGGAAAGTCTGCTGGTTC
Db      62 CGCAGAACTACTACAGCAGCCAGCTGAGAAAGTTGAGGAAAGTCTGCTGGTTC
Qy      142 TGCAGACGCGATGATACCTGACGCCGAAATAAACATCGCCCTTCTGCTTCACTGT
Db      122 TGCAGACGCGATGATACCTGACGCCGAAATAAACATCGCCCTTCTGCTTCACTGT
Qy      202 GAAAGGCGACGTGA-AGATCTCGCGCTGGATTTATCACTGACAGTAAACAAGTAT
Db      182 GAAAGGCGACGTGAAGATCTCGCGCTGGATTTATCACTGACAGTAAACAAGTAT
Qy      261 TCATGCTCATGCTATCTGTTGGCACTGATACAGAAACCAACAATTGACAGTTGTTG
Db      242 TCATGCTCATGCTATCTGTTGGCACTGATACAGAAACCAACAATTGACAGTTGTTG
Qy      321 GAGGGGTGTTGCACTTGTGACAGCAGTATGCTGCTTGGCAGCGGGCCCTTATTTACC
Db      302 GAGGGGTGTTGCACTTGTGACAGCAGTATGCTGCTTGGCAGCGGGCCCTTATTTACC
Qy      381 GGAAGCTTCTGTTCAATCCAGCGGCTCTTACCAAGAAAGCCTGTGCAATGAAAGAAAG
Db      362 GGAAGCTTCTGTTCAATCCAGCGGCTCTTACCAAGAAAGCCTGTGCAATGAAAGAAAG
Qy      441 AAGTTTGTATTTATTTATTTATTTAGTTGATGATTAAGTATTAACATATTTCTGTA
Db      422 AAGTTTGTATTTATTTATTTATTTAGTTGATGATTAAGTATTAACATATTTCTGTA
Qy      501 TTCTTCCAAAAA 519
Db      482 TTCTTCCAAAAA 500

```

RESULT 13
AAx15929
ID AAX15929 standard; cDNA; 467 BP.

AAx15929;

DT 12-JUN-2000 (first entry)

DE Human protein clone HP10357 full length coding sequence.

KM Human protein; hydrophobic domain; nutritional source; haematopoiesis;
KM cytokine production; cell proliferation; cell differentiation;
KM immune deficiency; infectious disease; autoimmune disorder; asthma;
KM multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
KM allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
KM nervous system disorder; Alzheimer's disease; Parkinson's disease;
KM Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
KM systemic cytokine damage; tissue differentiation; contraceptive; stroke;
KM coagulation disorder; myocardial infarction; inflammatory condition;
KM septic shock; sepsis; leukaemia; reperfusion injury; arthritis; tumour;
KM nephritis; therapy; ss.

XX Homo sapiens.

XX WO200005367-A2.

PN 03-FEB-2000.

PD 22-JUL-1999; 99WO-JP03929.

PR 24-JUL-1998; 98JP-0208820.

PR 07-AUG-1998; 98JP-0224105.

PR 25-AUG-1998; 98JP-0238116.
PR 09-SEP-1998; 98JP-0254736.
PR 29-SEP-1998; 98JP-0275505.
XX
XX (SAGA) SAGAMI CHEM RES CENT.
PA (PROT-) PROTEGENE INC.
XX
XX Kato S, Kimura T;
XX
XX WPI; 2000-182694/16.
DR P-PSDB; AAY94861.
XX
XX Novel human proteins having hydrophobic domains useful for treating
PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
XX
PS Claim 4; Page 228; 351pp; English.
XX
XX This sequence encodes a human protein of the invention, which has
CC hydrophobic domains. The DNA sequences can be used as a probe or as a
CC genetic marker. The protein can also be used as a marker, and to identify
CC potential genetic disorders. The DNA and protein can also be used as
CC nutritional sources or supplements. The protein exhibits cytokine, cell
CC proliferation, cell differentiation activities and induces production of
CC other cytokines in certain cell populations. The protein also exhibits
CC immune stimulating or immune suppressing activity. It can be used in the
CC treatment of various immune deficiencies and disorders, and to treat
CC infectious diseases caused by viral, bacterial, fungal or other
CC infections. The protein is also used for treating autoimmune disorders
CC such as multiple sclerosis, systemic lupus erythematosus, and Rheumatoid
CC arthritis. It is also useful in the treatment of allergic reactions and
CC conditions such as asthma, and in immune suppression after organ
CC transplantation. The protein is useful in regulation of haematopoiesis
CC and consequently in the treatment of myeloid or lymphoid cell
CC deficiencies. It is also used in compositions for tissue growth or
CC regeneration. The protein is also used in the treatment of osteoporosis
CC or osteoarthritis and in the treatment of periodontal disease and other
CC tooth repair processes. The protein is used in the treatment of nervous
CC system disorders such as Alzheimer's disease, Parkinson's disease, and
CC Huntington's disease. They are useful for protection or regeneration and
CC treatment of lung or liver fibrosis, reperfusion injury in various
CC tissues, and conditions resulting from systemic cytokine damage. They are
CC also used for promoting or inhibiting tissue differentiation. They are
CC also used as contraceptives since they exhibit activin or inhibin related
CC activities and as a fertility inducing therapeutic. They are used for
CC treating various coagulation disorders and in treatment and prevention of
CC conditions resulting from coagulation activities e.g. myocardial
CC infarction or stroke. They also acts as receptors, receptor ligands or
CC inhibitors or agonists of receptor/ligand interactions. They are used to
CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
CC reperfusion injury, arthritis, and nephritis. They can be used to
CC prevent tumours.
XX
XX Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other;
SQ
Query March 87.2%; Score 465.4; DB 21; Length 467;
Best Local Similarity 99.8%; Pred. No. 2.1e-92;
Matches 466; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 39 AGGGGAGGGCGGCTCCCGCGGCGGTGCTCTATCGCTTGCGAAGACTTACTGAGG 98
DB 1 AGGGGAGGGCGGCTCCCGCGGCGGTGCTCTATCGCTTGCGAAGACTTACTGAGG 60
QY 99 CAGGCACTGAGAGAGAGTGGAGGAAGTGTCTGCTGGGTCTGCGAGAGCCGATGATA 158
DB 61 CAGCACTGAGAGAGTGGAGGAAGTGTCTGCTGGGTCTGCGAGAGCCGATGATA 120
QY 159 ACGTGACCGGCAAAATATAAATCATGCGCCCTCTGCTTCAAGTGTAAAGGCCACGTGAAGA 218
DB 121 ACGTGACCGGCAAAATATAAATCATGCGCCCTCTGCTTCAAGTGTAAAGGCCACGTGAAGA 180
QY 219 TGCTGGCGCTGGATTTATCAACTCACTGTGTACAGAGATTTGATCTCATCTGATCTG 278
|||||

DB 181 TGCTGGCGCTGGATTTATCAACTCACTGTGTAAACAACAGATTTCATGCTCATCTG 240
QY 279 TGTGGCACTGATACAGAAACCAACAATTTGACAGTTGGTGGAGGGTGTGGCACTTG 338
DB 241 TGTGGCACTGATACAGAAACCAACAATTTGACAGTTGGTGGAGGGTGTGGCACTTG 300
QY 339 TGAACAGATATGCTGTCTTGGCCGAGGGGCCCTTATTTTACCGGAAGCTTGTTCATC 398
DB 301 TGACAGAGATATGCTGTCTTGGCCGAGGGGCCCTTATTTTACCGGAAGCTTGTTCATC 360
QY 399 CCAAGCGGCTCTTACCGAAGAAACCTGTGATGATAAAAAAGAGTTTGTATTTTATA 458
DB 361 CCAAGCGGCTCTTACCGAAGAAACCTGTGATGATAAAAAAGAGTTTGTATTTTATA 420
QY 459 TTACTTTTATGTTGATTAAGTATTAACATATTTCTGATCTT 505
DB 421 TTACTTTTATGTTGATTAAGTATTAACATATTTCTGATCTT 467
RESULT 14
ABK36006
ID ABK36006 standard; cDNA; 439 BP.
XX
XX ABK36006;
AC
XX 08-MAY-2002 (first entry)
DT
XX
DE cDNA sequence #397 encoding novel human secreted protein.
XX
XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;
XX immune deficiency disorder; blood disorder; inflammatory disorder;
XX infectious disorder; allergic condition; neurodegenerative disorder;
XX liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
XX tumour; cancer; hepatotropic; immunosuppressive; antineutlastic; gene; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200177289-A2.
XX
XX 18-OCT-2001.
PD
XX
XX 29-MAR-2001; 2001WO-US10332.
PF
XX
XX 06-APR-2000; 2000US-195605P.
PR
XX
XX (GENY) GENETICS INST INC.
PA
XX
XX Jacobs K, McCoey JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Agostino MJ, Bowman MR, Spaulding V, Wong GG;
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulkota K, Graham JR;
XX
XX WPI; 2002-179322/23.
DR
XX
XX Six hundred and twenty three polynucleotides derived from a variety of
PT human tissue sources which encode secreted proteins, useful for
PT treating immune deficiencies and disorders such as autoimmune disorders
PT
XX
XX Claim 1; Page 296-297; 393pp; English.
PS
XX
XX The present invention relates to the isolation of novel cDNA sequences
CC which encode human secreted proteins. The cDNA sequences have been
CC derived from a variety of human tissues. The invention also provides
CC a method for producing proteins from these polynucleotide sequences.
CC The proteins are useful for identifying compounds that modulate their
CC activity and production. The sequences of the invention are
CC useful for treating diseases such as hyperproliferative disorders
CC (e.g. cancer), immune deficiency disorders (e.g. severe combined
CC immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
CC sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
CC disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),
CC allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
CC Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.

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OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 02:39:42 ; Search time 2072 Seconds

(without alignments)
6263.798 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534
Sequence: 1 gtcccaatcgaagtgag.....aaaaaaaaaaaaa 534

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: em_esthum:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_hic:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: em_gss_hum:
18: em_gss_inv:
19: em_gss_pln:
20: em_gss_vit:
21: em_gss_fun:
22: em_gss_mam:
23: em_gss_mus:
24: em_gss_pro:
25: em_gss_rod:
26: em_gss_phg:
27: em_gss_vtl:
28: gb_gss1:
29: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	510.2	95.5	548	13	BUS32309
2	507.4	95.0	552	14	CB993661
3	505.8	94.7	524	10	BG705303
4	501.8	94.0	519	13	BX091668

Result No.	Score	Query Match	Length	ID	Description
5	492.4	92.2	528	13	BUS99247
6	492.4	92.2	562	10	BG249994
7	491.8	92.1	510	10	BF399486
8	487	91.2	781	10	BG529072
9	485.4	90.9	487	12	BM472086
10	485.4	90.9	526	13	BUS66499
11	482.4	90.3	534	10	BG311757
12	475	89.0	671	13	BK422104
13	474.4	88.8	1201	13	BK464689
14	469.8	88.0	510	13	BUS65721
15	469.2	87.9	955	13	BUI89908
16	468.2	87.7	529	10	BF691818
17	468	87.6	468	10	BF109912
18	467.6	87.6	930	10	BF203359
19	457.4	85.7	867	13	BUS33237
20	452	84.6	466	9	AI078580
21	446.8	83.7	917	13	BK436125
22	445	83.3	453	9	AI743235
23	438.8	82.2	820	13	BUS66814
24	432.4	81.0	533	9	AA429945
25	430.4	80.6	432	9	BUS64679
26	427.8	80.1	466	13	BUS64679
27	427	80.0	427	9	AA455042
28	422	79.0	423	9	AI128804
29	415.2	77.8	423	10	BG613984
30	413.8	77.5	432	9	AV759888
31	412.4	77.2	543	10	BG532587
32	411.8	77.1	1022	13	BUS36995
33	403	75.5	815	10	BF215121
34	402.6	75.4	409	9	AI826623
35	400.4	75.0	404	12	BM553628
36	399.4	74.8	402	9	AI989747
37	399	74.7	399	9	AA516431
38	394.4	73.9	396	9	AM183193
39	391	73.2	391	9	AI989739
40	386	72.3	386	9	AA911088
41	384.4	72.0	386	9	AA989129
42	381	71.3	395	9	AI141284
43	374.4	70.1	468	14	W52820
44	363	68.0	522	14	W38899
45	361.6	67.7	389	9	AA305052

ALIGNMENTS

RESULT 1
BUS32309 548 bp mRNA linear EST 13-SEP-2002
AGENCY 10202846 NIH_MGC 126 Homo sapiens CDNA clone
IMAGE:6557848 5', mRNA sequence.
ACCESSION BUS32309
VERSION BUS32309.1 GI:22842750
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
1 (bases 1 to 548)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCM2726 row: 1 column: 16
High quality sequence stop: 516.

FEATURES
source

Location/Qualifiers
1. 548
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6557848"
/tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_id="NIH_MGC_126"
/note="Vector: PDNR-LIB; Site 1: SfiI (ggccatcggc); Site 2: SfiI (ggccctcggc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AAGCAGTGTATCAACGAGAGTGGCCATTACGCCCGGG-3' and 5'-ATCTAGAGCGCGAGCGCGCAGATG-dt(30)NM-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Uedini, M.D., Ph.D. (NIH, NIH). Note: this is a NIH_MGC library."

BASE COUNT 169 a 107 c 134 g 133 t 5 others
ORIGIN

Query Match 95.5%; Score 510.2; DB 13; Length 548;
Best Local Similarity 98.5%; Pred. No. 3.3e-49;
Matches 512; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

15 GTGAAGCCGAGCTGGGCGAGAGTAGGGGAGGGGCTGCTCCGCGCGGTGGCT 74
1 GGGAAAGCCAGCTGGGCGAGAGTAGGGGAGGGGCTGCTCCGCGCGGTGGCT 60
75 ATCCGCTTCGAGAACTTACTCAGGAGCGACCTGAGAGATTGAGGAAAGTCTGCTG 134
61 ATCCGCTTCGAGAACTTACTCAGGAGCGACCTGAGAGATTGAGGAAAGTCTGCTG 120
135 CTGGGCTTCGAGAGCGGAGTAGATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTGCT 194
121 CTGGGCTTCGAGAGCGGAGTAGATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTGCT 180
195 TCAGTGTGAAGGCGCAGTGAAGATGCTGGGCTGGATATTATCACTCACTGGTAACA 254
181 TCAGTGTGAAGGCGCAGTGAAGATGCTGGGCTGGATATTATCACTCACTGGTAACA 240
255 CAGTATTCATGCTCATCTGATCTGTGTGGACATGATACAGAAACCAACATTTGACAG 314
241 CAGTATTCATGCTCATCTGATCTGTGTGGACATGATACAGAAACCAACATTTGACAG 300
315 TTGGTGAGGGGTTTGGCACTTGTGACAGAGATAGTCTGTCTTCCGACGGGGCCCTTA 374
301 TTGGTGAGGGGTTTGGCACTTGTGACAGAGATAGTCTGTCTTCCGACGGGGCCCTTA 360
375 TTTCACCGAAGCTTGTTCATCCACGGGCTCTTACAGAAAAGGCTGTGCATGAA 434
361 TTTCACCGAAGCTTGTTCATCCACGGGCTCTTACAGAAAAGGCTGTGCATGAA 420
435 AAAAAGAGTTTGTATTTTATTTATTTTATTTAGTTGATTAAGTATTAAATTT 494
421 AAAAAGAGTTTGTATTTTATTTATTTTATTTAGTTGATTAAGTATTAAATTT 480
495 TCTGTATTTCTCAAAAAAATTTTATTTTATTTTATTTAGTTGATTAAGTATTAAATTT 534
481 TCTGTATTTCTCAAAAAAATTTTATTTTATTTTATTTAGTTGATTAAGTATTAAATTT 520

RESULT 2
LOCUS CB993661 552 bp mRNA linear EST 01-MAY-2003

DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITL
JOURNAL
COMMENT

AGENCOURT_13617513 NIH_MGC_148 Homo sapiens cDNA clone
IMAGE:30333801 5', mRNA sequence.
CB993661
CB993661.1 GI:30288181
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 552)
NIH-MGC <http://mgs.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Straube, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Stefan Hansson
CDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.jnl.gov>
plate: NDAM353 row: a column: 10
High quality sequence stop: 552.

FEATURES
source

Location/Qualifiers
1. 552
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/db_xref="taxon:9606"
/clone="IMAGE:30333801"
/tissue_type="pre-eclampic placenta"
/lab_host="DH10B Tona"
/clone_id="NIH_MGC_148"
/note="Organ: Placenta; Vector: pBluescriptR; Site 1: all-XhoI; Site 2: BamH; Library is oligo-dT primed and directionally cloned using primer 5'-TTTTTTTTTTTTTTTT-3', size-selected for average insert size 2.3 kb and normalized to R0T 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC library."

BASE COUNT 151 a 119 c 146 g 136 t
ORIGIN

Query Match 95.0%; Score 507.4; DB 14; Length 552;
Best Local Similarity 99.8%; Pred. No. 6.8e-49;
Matches 508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

15 GTGAAGCCGAGCTGGGCGAGAGTAGGGGAGGGGCTGCTCCGCGCGGTGGCT 74
31 GGGAAAGCCAGCTGGGCGAGAGTAGGGGAGGGGCTGCTCCGCGCGGTGGCT 90
75 ATCCGCTTCGAGAACTTACTCAGGAGCGACCTGAGAGATTGAGGAAAGTCTGCTG 134
91 ATCCGCTTCGAGAACTTACTCAGGAGCGACCTGAGAGATTGAGGAAAGTCTGCTG 150
135 CTGGGCTTCGAGAGCGGAGTAGATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTGCT 194
151 CTGGGCTTCGAGAGCGGAGTAGATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTGCT 210
195 TCAGTGTGAAGGCGCAGTGAAGATGCTGGGCTGGATATTATCACTCACTGGTAACA 254
211 TCAGTGTGAAGGCGCAGTGAAGATGCTGGGCTGGATATTATCACTCACTGGTAACA 270
255 CAGTATTCATGCTCATCTGATCTGTGTGGACATGATACAGAAACCAACATTTGACAG 314
271 CAGTATTCATGCTCATCTGATCTGTGTGGACATGATACAGAAACCAACATTTGACAG 330
315 TTGGTGAGGGGTTTGGCACTTGTGACAGAGATAGTCTGTCTTCCGACGGGGCCCTTA 374

Db		331	TTGTGAGAGGGGTCTTTCACCTTGGA CAGCAGATATGCTGTCGCCAGCGGGCCCTTA	390
Qy		375	TTTACC GGAGCTTCTGTTCAATCCAGCGGCTCTTACCAAAAAAGCTTG CATGAA	434
Db		391	TTTTACCG GAAGCTTCTGTTCAATCCAGCGGCTCTTACCAAAAAAGCTTG CATGAA	450
Qy		435	AAAAAGAAGTTTGTAATTATTAATACTTTTAGTTTGATTAAGTATTAACAATAT	494
Db		451	AAAAGAAGTTTGTAATTATTAATACTTTTAGTTTGATTAAGTATTAACAATAT	510
Qy		495	TCTGTATTCTTCCAAAAA AAAAAAAAAA 523	
Db		511	TCTGTATTCTTCCAAAAA AAAAAAAAAA 539	
RESULT 3		BG705303	524 bp mRNA linear EST 07-MAY-2001	
LOCUS		60268780BRL NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820568 5'		
DEFINITION		mRNA sequence.		
ACCESSION		BG705303		
VERSION		BG705303.1 GI:13979504		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE		1 (bases 1 to 524)		
JOURNAL		NIH-MGC http://mgc.nci.nih.gov/.		
COMMENT		National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished		
		Contact: Robert Strausberg, Ph.D.		
		Email: cgapbs-rg@mail.nih.gov		
		Tissue Procurement: Miklos Palkovits, M.D., Ph.D.		
		cDNA Library Preparation: Michael J. Brownstein (NHGR1), Shizuki Toshiyuki and Piero Carninci (RIKEN)		
		cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		
		DNA Sequencing by: Incyte Genomics, Inc.		
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:		
		http://image.llnl.gov		
		Plate: LHAM10725 row: 0 column: 01		
FEATURES		High quality sequence stop: 521.		
source		Location/Qualifiers		
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		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/clone="IMAGE:4820568"		
		/tissue_type="hippocampus"		
		/lab_host="DH10B"		
		/clone_idb="NIH_MGC_95"		
		/note="Organ: brain; Vector: pBluescriptPR (modified pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gagcgaag...); Oligo-dT primed using primer 5'-ttttttttttttttv-3'', size-selected for average insert size 2.5 kb and normalized to ROL 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."		
BASE COUNT		142 a 113 c 138 g 131 t		
ORIGIN				
Query Match		94.7%; Score 505.8; DB 10; Length 524;		
Best Local Similarity		99.6%; Pred. No. 11e-48;		
Matches		507; Conservative 0; Mismatches 2; Indels 0; Gaps 0;		
Qy		15 GTGAAGCCGAGCTGGCGAGAGTAGTGGGAGGCGGTGCTCGCGCGGTGGCGGTTGCT	74	
Db		4 GGGAGCGCGAGTGGCGAGAGTAGTGGGAGGCGGTGCTCGCGCGGTGGCGGTTGCT	63	
Qy		75 ATGCGTTGCAGAACCTACTACGACGACGACGCTGAGAAAGTTGAGGAAAGTCTGCTG	134	

Db		64	ATGCTTTCGACAGACCGCATGATTAACGTGCAGACCAGCCTGAGAAGGTTGAGGGAAAGTGCTGCT	123
OY		135	CTGGGCTGTCAGACCGCATGATTAACGTGCAGACCAGCCGAAAATPAAACATGCCCTTCTGCT	194
Db		124	CTGGGCTGTCAGACCGCATGATTAACGTGCAGACCAGCCGAAAATPAAACATGCCCTTCTGCT	183
OY		195	TCAGTGTGAAGGCGACGTGAAGAAGTGTGGCGGCTGGAATTATTAACAATCACTGGTAACA	254
Db		184	TCACTGTGAAGGCGACGTGAAGAAGTGTGGCGGCTGGAATTATTAACAATCACTGGTAACA	243
OY		255	CAGATTTCATGCTCATGCTATCTGTGTGTGGCACCTGATPACAGAAACCAACAATTGACAG	314
Db		244	CAGATTTCATGCTCATGCTATCTGTGTGGCACCTGATPACAGAAACCAACAATTGACAG	303
Db		304	TTGGTGGAGGGGATGTGTGCACTGTGTGACAGAGATGCTGCTTCCGACGGGCGCTTGA	363
OY		375	TTTTACCGGAAGCTTCTGTTCATATCCGCGGCTCTTACAGAAAAAACCCTGTGATGAA	434
Db		364	TTTATCCGGAAGCTTCTGTTCATATCCGCGGCTCTTACAGAAAAAACCCTGTGATGAA	423
OY		435	AAAAAAGATTGTGATAATTATATATPACTTTTAGTTAGTTGATACAGATTAACATATT	494
Db		424	AAAAAAGATTGTGATAATTATATATPACTTTTAGTTAGTTGATACAGATTAACATATT	483
OY		495	TCTGTATTCTTCCAAAAAATTT	523
Db		484	TCTGTATTCTTCCAAAAAATTT	512
RESULT 4				
BX091668		519 bp	mRNA	EST 23-JAN-2003
LOCUS				
DEFINITION		BX091668 Soares ovary tumor NbhOT Homo sapiens cDNA clone		
ACCESSION		IMAGE998M041818 ; IMAGE:740523,		mRNA sequence.
VERSION		BX091668.1		GI:27822555
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
		Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE		1 (bases 1 to 519)		
AUTHORS		Ebert,L., Hell,O., Hennig,S., Neubert,P., Patsch,E., Peters,M.,		
		Radehof,U., Schneider,D. and Korn,B.		
TITLE		Human Unigeneset - RZPD3		
JOURNAL		Unpublished		
COMMENT		Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD: IMAGP998M041818. RZPDLIB: I.M.A.G.E. cDNA Clone Collection; Human Unigeneset - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CatalogCards/cgi-bin/showlib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel.: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAACGCTATGAC.		
FEATURES		Location/Qualifiers		
source		1..519		
		/organism="Homo sapiens"		
		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/clone="IMAGP998M041818 ; IMAGE:740523"		
		/sex="female"		
		/feature_type="ovarian tumor"		

BASE COUNT	143 a	109 c	133 g	134 t
ORIGIN	/lab_host="DHI0B_ampiicillin_resistant" /clone_id="Scares_ovary_tumor_NbHOT" /note="Organ: ovary; Vector: pRT13D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'- TGTTCACATCTGAAAGTGGAGCGGCCCGCGGCTTTTCTTTTCTTTTCTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRT13 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."			
Query Match	94.0%; Score 501.8; DB 13; Length 519;			
Best Local Similarity	99.8%; Pred. No. 3.1e-48;			
Matches 501; Conservative	0; Mismatches 1; Indels 0; Gaps 0;			
QY	23 GAGCTGGGCGGAAGTATAGGAGGAGGGGGGCTCCGCGCGGGTGGGTGCTATCGCTC 82			
DB	18 GAGCTGGGCGGAAGTATAGGAGGAGGGGGGCTCCGCGCGGGTGGGTGCTATCGCTC 77			
QY	83 GCAGAACCTACTCAGGACGCCAGCTGAGAAAGATTGAGGAAAGTCTGCTGGGCT 142			
DB	78 GCAGAACCTACTCAGGACGCCAGCTGAGAAAGATTGAGGAAAGTCTGCTGGGCT 137			
QY	143 GCAGACGGATGATACGTCGACGCCGGAATTAATTAATTCGCGCTTCTGCTCAGTGTG 202			
DB	138 GCAGACGGATGATACGTCGACGCCGGAATTAATTAATTCGCGCTTCTGCTCAGTGTG 197			
QY	203 AAAGGCCACATGAAATGCTGGGCTGGATATTAACAATCACTACGTGTAACAACGATATC 262			
DB	198 AAAGGCCACATGAAATGCTGGGCTGGATATTAACAATCACTACGTGTAACAACGATATC 257			
QY	263 ATGCTCATCGTATCTGTGTGTCGACCTGATACCAAGAAACCAACAATGACAGTGTGTCGA 322			
DB	258 ATGCTCATCGTATCTGTGTGTCGACCTGATACCAAGAAACCAACAATGACAGTGTGTCGA 317			
QY	333 GGGGTGTTTGCATTGTGTGACAGCAGTATGCTCTTGTGCGAGCGGGCCCTTATTTACCGG 382			
DB	318 GGGGTGTTTGCATTGTGTGACAGCAGTATGCTCTTGTGCGAGCGGGCCCTTATTTACCGG 377			
QY	333 AAGCTTCTGTTCAATCCACGGGCTCTTACCAAGAAAGCGCTGTGTCATGAAAAAGAA 442			
DB	378 AAGCTTCTGTTCAATCCACGGGCTCTTACCAAGAAAGCGCTGTGTCATGAAAAAGAA 437			
QY	443 GTTTGTATTTTATATTAATCTTTTATGTTTGAATCTAAGATTTAAACATATTTCTGATTT 502			
DB	438 GTTTGTATTTTATATTAATCTTTTATGTTTGAATCTAAGATTTAAACATATTTCTGATTT 497			
QY	503 CTTCCAAAAAAGAAAAA 524			
DB	498 CTTCCAAAAAAGAAAAA 519			
RESULT 5	BUS99247 528 bp mRNA linear EST 20-SEP-2002			
LOCUS	BUS99247			
DEFINITION	AGENCOURT_8908732 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6458265			
ACCESSION	BUS99247			
VERSION	BUS99247.1 GI:23251006			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
REFERENCE	1 (baeas 1 to 528)			
AUTHORS	NIH-MGC http://mgi.nci.nih.gov/.			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov			

```

FEATURES
source      I . 528
            Location/Qualifiers
            Tissue Procurement: NCI
            CDNA Library Preparation: Michael Brownstein Laboratory
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LNL at:
            http://image.lnl.gov
            Plate: LILCM641 row: h column: 06
            High quality sequence: 500.

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Query Match	Best Local Similarity	Matches	Conservative	Score	DB	Length	Indels	Gaps
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1	GGGAAGCCGAGCTGGCGCAGAAAGTAGGGGAGGCGCGTCTCCGCGCGGTGGCGGTGT	60						
15	GTGAAGCCGAGCTGGCGCAGAAAGTAGGGGAGGCGCGTCTCCGCGCGGTGGCGGTGT	74						
75	ATCCCTTGCGAGAACTTACTCAGCAGCAGCAGCTGAGAAAGTTGAGGAGAAAGTGTGTG	134						
61	ATCCCTTGCGAGAACTTACTCAGCAGCAGCAGCTGAGAAAGTTGAGGAGAAAGTGTGTG	120						
135	CTGGGCTGCGAGCGCGAGTGAATACGTGACAGCCGAGAAATTAACATGCGCCCTTGTCT	194						
121	CTGGGCTGCGAGCGCGAGTGAATACGTGACAGCCGAGAAATTAACATGCGCCCTTGTCT	180						
195	TCAGTGTGAAGGCGCAGCTGAAAGATGCTGGCGGTGGATTAATCAACTCAGTGTGAACA	254						
181	TCAGTGTGAAGGCGCAGCTGAAAGATGCTGGCGGTGGATTAATCAACTCAGTGTGAACA	240						
255	CAGTATTGATCTGATCGTATCTGTGTGTGGCAGCTGATACCAAGAAACCAACATTTGACAG	314						
241	CAGTATTGATCTGATCGTATCTGTGTGTGGCAGCTGATACCAAGAAACCAACATTTGACAG	300						
315	TTGGTGAAGGCGGTGTTTGCACTTGTGACAGAGTATGCTGTCTTGGCCGAGCGGGCCCTTGA	374						
301	TTGGTGAAGGCGGTGTTTGCACTTGTGACAGAGTATGCTGTCTTGGCCGAGCGGGCCCTTGA	360						
375	TTTACCGGAGACTTCTGTTCATATCCGACGGGTCTTACCAGAAAAGCCTGTGCAATGAAA	434						
361	TTTACCGGAGACTTCTGTTCATATCCGACGGGTCTTACCAGAAAAGCCTGTGCAATGAAA	420						
435	AAAAAGAGTTTGAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT	494						
421	AAAAAGAGTTTGAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT	480						

QY 495 TCTGTATCTTCCA 508
Db 481 TCTGTATCTTCCA 494

RESULT 6
LOCUS BG249994 962 bp mRNA linear EST 13-FEB-2001
DEFINITION 602362062F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:4470662 5', mRNA sequence.
ACCESSION BG249994
VERSION BG249994.1 GI:12759810
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 962)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: LLM10288 row: k column: 15
High quality sequence stop: 516.
Location/Qualifiers
1. 962
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/clone_id="NIH_MGC_90"
/note="Organ: liver; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC library."
BASE COUNT 334 a 199 c 288 g 141 t
ORIGIN

Query Match 92.2%; Score 492.4; DB 10; Length 962;
Best Local Similarity 99.6%; Pred. No. 2.3e-47;
Matches 504; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 29 GGGGAGAGTAGGGGAGGGGCTGCTCCGCCGGTGGCGGTGCTATCGCTTCGACAGAA 88
Db 1 GGGGAGAGTAGGGGAGGGGCTGCTCCGCCGGTGGCGGTGCTATCGCTTCGACAGAA 60

QY 89 CTTACTAGGACGACCTGAGAGAGATTGAGGGGAAATGCTGCTGGGCTTCGACAG 148
Db 61 CTTACTAGGACGACCTGAGAGAGATTGAGGGGAAATGCTGCTGGGCTTCGACAG 120

QY 149 GCGATGATACGCGACGACGCGGAAATGATGCGCCCTTCGCTCAGTGGGAAAGGC 208
Db 121 GCGATGATACGCGACGCGGAAATGATGCGCCCTTCGCTCAGTGGGAAAGGC 180

QY 209 CACGTGAAGATGCTGCGGCTGATATTTATCACTCTGTGTAACACAGATTATCTGCTC 268
Db 181 CACGTGAAGATGCTGCGGCTGATATTTATCACTCTGTGTAACACAGATTATCTGCTC 240

QY 269 ATGTATCTGTGTTGGACATGATACCGAAGAACCAACATTGACAGTTGGTGAAGGGGTG 328
Db 241 ATGTATCTGTGTTGGACATGATACCGAAGAACCAACATTGACAGTTGGTGAAGGGGTG 300

QY 329 TTGGCACTTTGACACAGCATATGCTGCTTCCGACGGGGCCCTTATTACCGGAAGCTT 388
Db 301 TTGGCACTTTGACACAGCATATGCTGCTTCCGACGGGGCCCTTATTACCGGAAGCTT 360

QY 389 CTGTTCAATCCAGCGGCTCTTACGAGAAAGCCGTGTCATGAAAGAAAGAGTTTG 448
Db 361 CTGTTCAATCCAGCGGCTCTTACGAGAAAGCCGTGTCATGAAAGAAAGAGTTTG 419

QY 449 TATTTTATTTACTTTTATTTAGTTTGTGATTAAGTATTAACATATTTCTGTATCTTCCA 508
Db 420 TATTTTATTTACTTTTATTTAGTTTGTGATTAAGTATTAACATATTTCTGTATCTTCCA 479

QY 509 AAAAAAAAAAAAAAAAAAAAAA 534
Db 480 CAAAAAAAAAAAAAAAAAAAAA 505

RESULT 7
LOCUS BF399486/c 510 bp mRNA linear EST 27-NOV-2000
DEFINITION UI-R-CAI-bjb-b-12-0-UI-61 UI-R-CAI Rattus norvegicus cDNA clone
UI-R-CAI-bjb-b-12-0-UI 3', mRNA sequence.
ACCESSION BF399486
VERSION BF399486.1 GI:11384494
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 510)
AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLY=A=Yes.
Location/Qualifiers
1. 510
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/mol_type="mRNA"
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/lab_host="DH10B (Life Technologies)"
/clone_id="UI-R-CAI"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CAI library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medulla, pons, midbrain, cerebral cortex, corpus striatum, testis, and hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
BASE COUNT 130 a 131 c 104 g 145 t
ORIGIN

REFERENCE 1 (bases 1 to 487)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM12328 row: a column: 12
High quality sequence stop: 486.

FEATURES
source

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/mol_type="mRNA"
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/clone="IMAGE:5576339"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: PCMV-SPORT6; Site 1: Nci1; Site 2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 135 a 103 c 121 g 128 t
ORIGIN

Query Match 90.9%; Score 485.4; DB 12; Length 487;
Best Local Similarity 99.8%; Pred. No. 2.3e-46;
Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 AGTAGGGGAGGCGCGTCTCCGCGCGGTGGCGGTGCTGATCGCTTCGAGAACCTACTC 95
DB 1 AGTAGGGGAGGCGCGTCTCCGCGCGGTGGCGGTGCTGATCGCTTCGAGAACCTACTC 60
QY 96 AGGAGCGCAGCTGGAAGAGTTGAGGGAAGTGTCTGCTGGGTTCGACAGCCGATGG 155
DB 61 AGGAGCGCAGCTGGAAGAGTTGAGGGAAGTGTCTGCTGGGTTCGACAGCCGATGG 120
QY 156 ATACGTCGACGCGAATAAATCAATGCGCCCTCTGCTGATGTAAGGCGCAGCTGA 215
DB 121 ATACGTCGACGCGAATAAATCAATGCGCCCTCTGCTGATGTAAGGCGCAGCTGA 180
QY 216 AGATGCTGCGGCTGATATTCATCACTGATCACTGTAACAAGATTCATGCTCATGTA 275
DB 181 AGATGCTGCGGCTGATATTCATCACTGATCACTGTAACAAGATTCATGCTCATGTA 240
QY 276 CTGTGTTGGCAGTATACAGAAACCAACATTTGACAGTTGTGAGAGGGGTGTTGCAC 335
DB 241 CTGTGTTGGCAGTATACAGAAACCAACATTTGACAGTTGTGAGAGGGGTGTTGCAC 300
QY 336 TTGTCAGACAGCTATGCTGCTTCCGACGGGGCCCTTATTTACCGAAGCTTGTGTC 395
DB 301 TTGTCAGACAGCTATGCTGCTTCCGACGGGGCCCTTATTTACCGAAGCTTGTGTC 360
QY 396 ATCCACGCGTCTTACCAAGAAAGCTGTGATGAAAGAAAGTTTGTAAATTTT 455
DB 361 ATCCACGCGTCTTACCAAGAAAGCTGTGATGAAAGAAAGTTTGTAAATTTT 420
QY 456 ATATTACTTTTAACTGATTAAGTATTAACATATTTCTGATTTCTTCAAAAAA 515
DB 421 ATATTACTTTTAACTGATTAAGTATTAACATATTTCTGATTTCTTCAAAAAA 480
QY 516 AAAAAA 522
DB 481 AAAAAA 487

RESULT 10
BUS66499 526 bp mRNA linear EST 16-SEP-2002
LOCUS BUS66499
DEFINITION AGENCOURT 10397961 NIH_MGC 141 Homo sapiens cDNA clone
IMAGE:6605733 5', mRNA sequence.

ACCESSION BUS66499
VERSION BUS66499.1 GI:22916799
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 526)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
Plate: LLM2850 row: d column: 21
High quality sequence stop: 494.

FEATURES
source

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/db_xref="taxon:9606"
/clone="IMAGE:6605733"
/tissue_type="mixed (pool of 40 RNAs)"
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/clone_lib="NIH_MGC_141"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggcccatatggcc); Site 2: SfiI (ggcgctcgccg); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
5'-AACGATGCTATCAAGCAGACAGTGGCCATACGGCGG-3' and
5'-ATCTAGAGGCCGAGGGGCGGCAATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.2-0.5 kb size fraction (other fractions present in NIH_MGC 142). Library created in the laboratory of M. Brownstein (NIH). Note: this is a NIH_MGC Library."

BASE COUNT 126 a 106 c 135 g 132 t 27 others
ORIGIN

Query Match 90.9%; Score 485.4; DB 13; Length 526;
Best Local Similarity 95.9%; Pred. No. 2.2e-46;
Matches 486; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 23 GAGCTGGGCGAAGTAGGGGAGGCGGTGCTCCGCGCGGTGGCTTATCGCTTC 82
DB 4 GAGCTGGGCGAAGTAGGGGAGGCGGTGCTCCGCGCGGTGGCTTATCGCTTC 63
QY 83 GCAGAACTTACTCAGGACGACCTAGAGAGATTTAGGGAAGTGTGCTGGGTCT 142
DB 64 GCAGAACTTACTCAGGACGACCTAGAGAGATTTAGGGAAGTGTGCTGGGTCT 123
QY 143 GCAGAGCGATGATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTCAGGTG 202
DB 124 GCAGAGCGATGATTAAGTGCAGCGGAAATTAACATGCGCCCTTCTCAGGTG 183
QY 203 AAAGGCCAGTGAAGATGCTGCGGCTGGATTTATCAACTGTTAACAAGATTTG 262

Db 184 AAGGCCAGTGAAGATGCTGGCGGTGATATTAATCACTGATGTAACAAGATATTC 243
Qy 263 ATGCTCATGATATCTGTGTGGCACTGATACAGAAACCAACAATTGACAGTTGTGGA 322
Db 244 ATGCTCATGATATCTGTGTGGCACTGATACAGAAACCAACAATTGACAGTTGTGGA 303
Qy 323 GGGGTGTTTGACCTGTGTGACAGCAGTATGCTGTTCGCGACGGGGCCCTTATTTACCGG 382
Db 304 GGGGTGTTTGACCTGTGTGACAGCAGTATGCTGTTCGCGACGGGGCCCTTATTTACCGG 363
Qy 383 AAGCTTCTGTTCAATCCAGAGGGTCTTACCAAGAAAAAGCTGTGTGCAATGAAAAAGAA 442
Db 364 AAGCTTCTGTTCAATCCAGAGGGTCTTACCAAGAAAAAGCTGTGTGCAATGAAAAAGAA 423
Qy 443 GTTTGTAATTTATTAATTAATTTAGTTGATTAAGTAAATATTTCTGATTT 502
Db 424 GTTTGTAATTTATTAATTAATTTAGTTGATTAAGTAAATATTTCTGATTT 483
Qy 503 CTTCCAAAAAAGAAAAAAGAAAAA 529
Db 484 CTTCCAAAAAAGAAAAAAGAAAAA 510

RESULT 11
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LOCUS 602299819P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4394093 5',
DEFINITION mRNA sequence.
ACCESSION Bg031757
VERSION Bg031757.1 GI:12422364
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 534)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
http://image.llnl.gov
Plate: L1AM10089 row: e column: 06
High quality sequence stop: 446.
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1. 534
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/clone_lib="NIH_MGC_87"
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Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

BASE COUNT 163 a 108 c 132 g 131 t
ORIGIN

Query Match 90.3%; Score 482.4; DB 10; Length 534;
Best Local Similarity 98.2%; Pred. No. 4.8e-46;
Matches 499; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

Qy 30 GCGAAGAACTAGGAGGCGGTGCTCCGCCGGGTGGCGGTGCTGATGCTTCGAGAAC 89
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Db 1 GCGAAGAACTAGGAGGCGGTGCTCCGCCGGGTGGCGGTGCTGATGCTTCGAGAAC 60
Qy 90 CTATCTCAGGAGCAGCTGAGAGAGTTGAGGAGAAAGTGTCTGTCTGCTGCAGACG 149
Db 61 CTATCTCAGGAGCAGCTGAGAGAGTTGAGGAGAAAGTGTCTGTCTGCTGCAGACG 120
Qy 150 CGATGATTAACGTGACAGCCGAAATTAACATGCCCCCTTCTGCTTCACTGTGAAAGCC 209
Db 121 CGATGATTAACGTGACAGCCGAAATTAACATGCCCCCTTCTGCTTCACTGTGAAAGCC 180
Qy 210 ACGTGAAGATGCTGGCGCTGGATATTAATCACTGATGATTAACAAGATTCATGCTCA 269
Db 181 ACGTGAAGATGCTGGCGCTGGATATTAATCACTGATGATTAACAAGATTCATGCTCA 240
Qy 270 TCGATCTGTGTGGCACTGATACCAAGAAACCAACATTTGACAGTTGTGTGAGGGGTGT 329
Db 241 TCGATCTGTGTGGCACTGATACCAAGAAACCAACATTTGACAGTTGTGTGAGGGGTGT 300
Qy 330 TTGCACTTGTGACAGCAGTATGCTGTCTTCCGACGGGGCCCTTATTTACCGGAAGCTTC 389
Db 301 TTGCACTTGTGACAGCAGTATGCTGTCTTCCGACGGGGCCCTTATTTACCGGAAGCTTC 360
Qy 390 TGTTCATCCGACGGGCTTACCAAGAAAGCTGTGATGAAAAAGAGTTTGT 449
Db 361 TGTTCATCCGACGGGCTTACCAAGAAAGCTGTGATGAAAAAGAGTTTGT 420
Qy 450 AATTTATATTAATTTTATTTAGTTGATTAAG--TATTAACAATATTTCTGATTTCTTC 506
Db 421 AATTTATATTAATTTTATTTAGTTGATTAAGTTATTTAAACATATTTCTGATTTCTTT 480
Qy 507 CAAAAAAGAAAAAAGAAAAAAGAAAAA 534
Db 481 CAAAAAAGAAAAAAGAAAAAAGAAAAA 508

RESULT 12
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LOCUS BX422104 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
DEFINITION clone CS0DH007YB16 5-PRIME, mRNA sequence.
ACCESSION BX422104
VERSION BX422104.1 GI:30647202
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 671)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8312.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DH007DA08QPL&cluster=8312.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DH007DA08QPL.
Location/Qualifiers
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/cell_line="JURKAT CELL LINE"
/note="Vector: pCMVSPORT_6; 1st strand cDNA was primed

REFERENCE	1 (bases 1 to 510)
AUTHORS	NIH-MGC http://mgc.ncbi.nlm.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

CGNA Library Preparation: Michael Brownstein Laboratory
 CGNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LINC2847 row: b column: 18
 High quality sequence stop: 482.
 Location/Qualifiers

FEATURES	Location/Qualifiers
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1. .510
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone IMAGE:6604530"
/lab_host="DH10B (T1-phage-resistant)"
/clone_1ib="NIH MGC 141"
/notes="Vector: pDNR-LIB; Site.1: Sfil (ggccatcatggcgc);
Site.2: Sfil (ggcgcctggcgc); "double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%
ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGCAGTGTGATTCACCGCAGAGTGGCATTTAGCGCGGG-3' and
5'-ATCTTAGAGCGCGAGCGCGCGCAGCATG-dT(30)NN-3'. Full-length
enriched library was constructed using the Clontech
creator SMART kit and size-selected to contain the 0.2-0.5
kb size fraction (other fractions present in NIH MGC 142).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH MGC library."

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Query Match	88.0%	Score 469.8	DB 13	Length 510
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				Gaps 0

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QY	100	AGCCAGCTGAGAGAGTTGAGGGAAAGTGTCTGCTGGGTCTGCAGACGCGATGATAA	159
Db	65	AGCCAGCTGAGAGAGTTGAGGGAAAGTGTCTGCTGGGTCTGCAGACGCGATGATAA	124
QY	160	CGTGACGCCGAAATTAATAACATCGCCGCTTCGTCTAGTGTGAAGAAGCCAGTAAGAT	219
Db	125	CGTGACGCCGAAATTAATAACATCGCCGCTTCGTCTAGTGTGAAGAAGCCAGTAAGAT	184
QY	220	GCTGGCGGTGAGTATTATCAACTCACTGTGAACAACAGATTCACTCATGTATCTGT	279
Db	185	GCTGGCGGTGAGTATTATCAACTCACTGTGAACAACAGATTCACTCATGTATCTGT	244
QY	280	GTTGGCACTGATACCGAANAACACAACATTGACATTTGTGGAGGGGCTTTGCATCTGT	339
Db	245	GTTGGCACTGATACCGAANAACACAACATTGACATTTGTGGAGGGGCTTTGCATCTGT	304
QY	340	GACAGCAGTATGCTGCTTGTGCGACGCGGGCCCTTATTTACGGGAAGCTTCTGTTCAATCC	399
Db	305	GACAGCAGTATGCTGCTTGTGCGACGCGGGCCCTTATTTACGGGAAGCTTCTGTTCAATCC	364
QY	400	CAGCGGTCTTACCGAANAAGCTGTGATGAAAAAAGAGTTTGTATTTTATAT	459

Db 365 CACGGGCTCTACGAGAAAAACCGTCGATGAGAAAAAACAAGATTGTAATTAT 424

Dy 460 TACTTTTGTGTTGATCTACTATATTAACATATTCTGATCTTCGCAAAAAA 519

425 TACTTTTGTGTTGATCTACTATATTAACATATTCTGATCTTCGCAACANNNNNN 484

Qy	520	AAAAAAAAAAAA	533
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RESULT	15
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DEFINITION	AGENCOURT 803697 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6167613 5', mRNA sequence.

ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
BU189908	BU189908.1	GI:22703892 EST.	Homo sapiens	Homo sapiens (human)
			Homo sapiens	Homo sapiens

REFERENCE	1 (bases 1 to 855)
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished
COMMENT	Contact: Robert Strausberg, Ph.D.

FEATURES
source
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC/DCDT/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LLAM13529 row: m column: 22
 High quality sequence crop: 655.
 Location/Qualifiers
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BASE COUNT	190 a	200 c	257 g	206 t	2 others
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QY	99	CAGCGAGCTGAGAGAGTTGAGGAGAAAGTGTGCTGCTGGGCTCTGCACAGCGATGATTA	158	
Db	61	CAGCGAGCTGAGAGAGTTGAGGAGAAAGTGTGCTGCTGGGCTCTGCACAGCGATGATTA	120	
QY	159	ACGTGCAGCCGAAATAAACAATGCGCCCTTCTGCTTCAGTGTGAAAGCCACGTGAAGA	218	
Db	121	ACGTGCAGCCGAAATAAACAATGCGCCCTTCTGCTTCAGTGTGAAAGCCACGTGAAGA	180	
QY	219	TGCTGCGGCTGGATATATATCAACTCACTGCTGAACAACAGTATTCATGCTATCGATATCG	278	
Db	181	CGCTGCGGCTGGATATATATCAACTCACTGCTGAACAACAGTATTCATGCTATCGATATCG	240	


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Qy 279 TGTGGCACTGATACCAAGAAACCAACATGACAGTGGATGAGGGGTGTTGCACTTG 338
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Qy 399 CCAGCGGTCCTTACCAAGAAAGCCCTGTCATGAAAAAGAAAGTTTGTAAATTTATA 458
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Db 361 CCAGCGGTCCTTACCAAGAAAGCCCTGTCATGAAAAAGAAAGTTTGTAAATTTATA 420
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Qy 459 TTACTTTTAACTTGAATTAAGTATTAAATATTTCTGATTTCTTCCAAAA 512
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Search completed: January 31, 2004, 04:09:42
 Job time : 2077 secs

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QY 135 CTGGGCTGACAGACGCGATGATAGCGAGCCGAAATTAACATGCCCCCTTGCT 194
Db 127 CTGGGCTGACAGACGCGATGATAGCGAGCCGAAATTAACATGCCCCCTTGCT 186
QY 195 TCAGTGTGAAGGCGACGTGAAGATGCTGCGGTGATATTATCACTGCTGTAACA 254
Db 187 TCAGTGTGAAGGCGACGTGAAGATGCTGCGGTGATATTATCACTGCTGTAACA 246
QY 255 CAGATTTCATGCTATGATATCTGTGTTGGCATGATACCGAAGAACCAACATTGACAG 314
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QY 315 TTGGTGAAGGGGTTTGGCATGTTGACAGCAGATGCTGCTGCGAGCGGGCCCTTA 374
Db 307 TTGGTGAAGGGGTTTGGCATGTTGACAGCAGATGCTGCTGCGAGCGGGCCCTTA 366
QY 375 TTACCGGAAGCTTCTGTTCAATCCAGCGGTCTCTTACAGAAAGCCTGTGATGAA 434
Db 367 TTACCGGAAGCTTCTGTTCAATCCAGCGGTCTCTTACAGAAAGCCTGTGATGAA 426
QY 435 AAAAAGAGTTTGTATTTATATTAATTTTGTGATGATGATTTAAATTAATTT 494
Db 427 AAAAAGAGTTTGTATTTATATTAATTTTGTGATGATGATTTAAATTAATTT 486
QY 495 TCTGATTTCTTCAAAAAA 522
Db 487 TCTGATTTCTTCAAAAAA 514

RESULT 2

US-09-149-476-98

Sequence 98. Application US/09149476.

Patent No. 6420526

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 186 Human Secreted proteins

FILE REFERENCE: P2002P1

CURRENT APPLICATION NUMBER: US/09/149,476

CURRENT FILING DATE: 1998-09-08

EARLIER APPLICATION NUMBER: PCT/US98/04493

EARLIER FILING DATE: 1998-03-06

EARLIER APPLICATION NUMBER: 60/040,162

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,333

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/038,621

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,626

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,334

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EARLIER APPLICATION NUMBER: 60/040,336

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/040,163

EARLIER FILING DATE: 1997-03-07

EARLIER APPLICATION NUMBER: 60/047,600

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,615

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,597

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,502

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,633

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,583

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,617

EARLIER FILING DATE: 1997-05-23

EARLIER APPLICATION NUMBER: 60/047,618

EARLIER FILING DATE: 1997-08-22

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EARLIER APPLICATION NUMBER: 60/043,569
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EARLIER APPLICATION NUMBER: 60/043,311
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,671
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EARLIER APPLICATION NUMBER: 60/043,674
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,669
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,312
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EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,886
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,877
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EARLIER APPLICATION NUMBER: 60/056,889
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,893
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,878
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,662
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,872
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,882

EARLIER APPLICATION NUMBER: 60/056,637
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,903
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,888
 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
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 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,910
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,864
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 EARLIER APPLICATION NUMBER: 60/056,631
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,845
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/047,595
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,599
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/047,588
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 EARLIER APPLICATION NUMBER: 60/047,585
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 EARLIER FILING DATE: 1997-05-23
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 EARLIER APPLICATION NUMBER: 60/047,614
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/043,578
 EARLIER FILING DATE: 1997-04-11
 EARLIER APPLICATION NUMBER: 60/043,576
 EARLIER FILING DATE: 1997-04-11
 EARLIER APPLICATION NUMBER: 60/047,501
 EARLIER FILING DATE: 1997-05-23
 EARLIER APPLICATION NUMBER: 60/043,670
 EARLIER FILING DATE: 1997-04-11
 EARLIER APPLICATION NUMBER: 60/056,632
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,664
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,876
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,881
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,909
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,875
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,862
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,887

EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/056,908
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/048,964
 EARLIER FILING DATE: 1997-06-06
 EARLIER APPLICATION NUMBER: 60/057,650
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/056,884
 EARLIER FILING DATE: 1997-08-22
 EARLIER APPLICATION NUMBER: 60/057,669
 EARLIER FILING DATE: 1997-09-05
 EARLIER APPLICATION NUMBER: 60/049,610
 EARLIER FILING DATE: 1997-06-13
 EARLIER APPLICATION NUMBER: 60/061,060
 EARLIER FILING DATE: 1997-10-02

Query Match 91.1%; Score 486.6; DB 4; Length 504;
 Best Local Similarity 99.0%; Pred. No. 5.9e-115;
 Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 21 CCGAGCTGGGCGAGAGTAGGGGAGGCGGTCTCCGCCGGGTGGCGTGTATCGT 80
 DB 1 CCGAGCTGGGCGAGAGTAGGGGAGGCGGTCTCCGCCGGGTGGCGTGTATCGT 59
 QY 81 TCGCAGAACTTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAAAGTGTCTGGGT 140
 DB 60 TCGCAGAACTTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAAAGTGTCTGGGT 119
 QY 141 CTGCAACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 200
 DB 120 CTGCAACGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 179
 QY 201 TGAAGGCGAGGAT 260
 DB 180 TGAAGGCGAGGAT 239
 QY 261 TCATGCTCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 320
 DB 240 TCATGCTCATGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 299
 QY 321 GAGGGGTTTGCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 380
 DB 300 GAGGGGTTTGCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 359
 QY 381 GGAAGCTTGTTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 440
 DB 360 GGAAGCTTGTTCATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 419
 QY 441 AAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 500
 DB 420 AAGTTTGTATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 479
 QY 501 TTCTTCCAAAAA 525
 DB 480 TTCTTCCAAAAA 504

RESULT 3
 US-09-149-476-252
 Sequence 252, Application US/09149476
 Patent No. 6420526
 GENERAL INFORMATION:
 APPLICANT: Rosen et al.
 TITLE OF INVENTION: 186 Human Secreted proteins
 FILE REFERENCE: P2002P1
 CURRENT APPLICATION NUMBER: US/09/149,476
 EARLIER FILING DATE: 1998-09-08
 EARLIER APPLICATION NUMBER: PCT/US98/04493
 EARLIER FILING DATE: 1998-03-06
 EARLIER APPLICATION NUMBER: 60/040,162
 EARLIER FILING DATE: 1997-03-07
 EARLIER APPLICATION NUMBER: 60/040,333
 EARLIER FILING DATE: 1997-03-07

EARLIER	APPLICATION NUMBER: 60/038, 621
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EARLIER	FILING DATE: 1997-05-23
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EARLIER	FILING DATE: 1997-05-23
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EARLIER	FILING DATE: 1997-04-11
EARLIER	APPLICATION NUMBER: 60/043, 313

[illegible]

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EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
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EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
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EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Query Match 89.6%; Score 478.6; DB 4; Length 506;
Best Local Similarity 97.4%; Pred. No. 6.4e-113;
Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;

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QY 37 GTAGGGAAGGCGGCTCCCGCGGCGGCTTCTATGCTTCCGAACTACTCA 96
D 2 GCAGGATTTGGCCGAGGCCGCCGCGGCGGCTTCTATGCTTCCGAACTACTCA 61
QY 97 GGCAGCAGCTGAGAAGAGTGAAGGAAGTGTGCTGGTCTGGTGAAGGCGCATGGA 156
D 62 GGCAGCAGCTGAGAAGAGTGAAGGAAGTGTGCTGGTCTGGTGAAGGCGCATGGA 121
QY 157 TAACTGAGCGCGAATAAACAATCGCCCTTCTGCTTCACTGTAAGGCGCATGGA 216
D 122 TAACTGAGCGCGAATAAACAATCGCCCTTCTGCTTCACTGTAAGGCGCATGGA 181
QY 217 GATGCTGGCTGATATTAATCACTCACTGTAACAACAGTATTCATGCTCATGATC 276
D 182 GATGCTGGCTGATATTAATCACTCACTGTAACAACAGTATTCATGCTCATGATC 241
QY 277 TGTGTTGGCACTGATACAGAAACCAACAATGACAGTTGGTGAAGGCGGTTGCACT 336
D 242 TGTGTTGGCACTGATACAGAAACCAACAATGACAGTTGGTGAAGGCGGTTGCACT 301
QY 337 TGTGACAGCACTATGCTGCTTGGCGACGCGGCGCTTATTTACGGAAGCTTCTGTTCAA 396
D 302 TGTGACAGCACTATGCTGCTTGGCGACGCGGCGCTTATTTACGGAAGCTTCTGTTCAA 361
QY 397 TCCGAGCGGCTCTTAACGAAAAAGCTGTGCAATGAAAAAAGAGTTTGTATTTTA 456
D 362 TCCGAGCGGCTCTTAACGAAAAAGCTGTGCAATGAAAAAAGAGTTTGTATTTTA 421
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QY 457 TATTACTTTTACTTTGATGATCTAAGTATTAACATATTTCTGATCTTCCAAAAA 516
D 422 TATTACTTTTACTTTGATGATCTAAGTATTAACATATTTCTGATCTTCCAAAAA 481
QY 517 AAAAAAAAAAAAAAAAAA 533
D 482 AAAAAAAAAAAAAAAAAA 498

RESULT 4
US-09-663-600A-53
; Sequence 53: Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 53
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 199..288
; OTHER INFORMATION: Von Heijne matrix
; OTHER INFORMATION: score 5.59999990463257
; NAME/KEY: polyA_signal
; LOCATION: 464..469
; NAME/KEY: polyA_site
; LOCATION: 489..500
; NAME/KEY: misc_feature
; LOCATION: 197..412
; OTHER INFORMATION: homology
; OTHER INFORMATION: id: AA429945
; OTHER INFORMATION: est
; NAME/KEY: misc_feature
; LOCATION: 61..195
; OTHER INFORMATION: homology
; OTHER INFORMATION: id: AA429945
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; NAME/KEY: misc_feature
; LOCATION: 197..412
; OTHER INFORMATION: homology
; OTHER INFORMATION: id: AA455042
; OTHER INFORMATION: est
; NAME/KEY: misc_feature
; LOCATION: 61..195
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NAME/KEY: misc feature
LOCATION: 40..195
OTHER INFORMATION: homology
OTHER INFORMATION: id :#19506
OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 9..10,12
OTHER INFORMATION: n=a, 5, c or t

US-09-663-600A-53

Query Match 87.4%; Score 466.8; DB 4; Length 500;
Best Local Similarity 97.8%; Pred. No. 6,5e-110;
Matches 488; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Query 23 GAGCTGGCGGAGAAATTAAGGGAGGGCGGTCTCCCGCGCGGTGGCGG-TTGCTATCCCTT 81
Db 2 GAGCTGTNNCCNNAAGTATAGGGAGGGCGGTCTCCCGCGGTGGCGGDBHTGCTATCCCTT 61
Query 82 CGCAAACTCTACTCAGGCGAGCGAGCTGAGAGAGTTGAGGGAAGTCTCTCTCGGGTC 141
Db 62 CGCAAACTCTACTCAGGCGAGCGAGCTGAGAGAGTTGAGGGAAGTCTCTCTCGGGTC 121
Query 142 TGCAGACGCGATGATGATTAACGTGCGAGCCGAAATTAACATCGCCCTTCTGCTTCACTGT 201
Db 122 TGCAGACGCGATGATTAACGTGCGAGCCGAAATTAACATCGCCCTTCTGCTTCACTGT 181
Query 202 GAAAGGCCACAGTGA-AGATGCTGCGGCTGATTTATCAACTACTGCTGTAACACAGTAT 260
Db 182 GAAAGGCCACAGTGAAGATGCTGCGGCTGATTTATCAACTACTGCTGTAACACAGTAT 241
Query 261 TCATGCTCATGCTATCTGTGTGGCACTGATACCAAGAACCAACATGACAGTGGTG 320
Db 242 TCATGCTCATGCTATCTGTGTGGCACTGATACCAAGAACCAACATGACAGTGGTG 301
Query 321 GAGGGGTGTTTGCACTTGTGACAGAGTATGCTGTCTTGCGGAGCGGGCCCTTATTTACC 380
Db 302 GAGGGGTGTTTGCACTTGTGACAGAGTATGCTGTCTTGCGGAGCGGGCCCTTATTTACC 361
Query 381 GGAAGCTTCTGTTCATCCAGCGGCTCTTACCAAGAAAAAGCTGTGCAATGAAAAAAG 440
Db 362 GGAAGCTTCTGTTCATCCAGCGGCTCTTACCAAGAAAAAGCTGTGCAATGAAAAAAG 421
Query 441 AAGTTTGTAATTTATATATCTTTTATGTAATGTAATTAACATATTTCTGTA 500
Db 422 AAGTTTGTAATTTATATATCTTTTATGTAATGTAATTAACATATTTCTGTA 481
Query 501 TTCTTCCAAAAAATTTTAAAAA 519
Db 482 TTCTTCCAAAAAATTTTAAAAA 500

RESULT 5
US-09-220-132-164/c
Sequence 164; Application US/09220132
Patent No. 6506807
GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
FILE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 60/068,821
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 164
LENGTH: 526
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)..(526)
OTHER INFORMATION: n = A,T,C or G
US-09-220-132-164

Query Match 87.2%; Score 465.8; DB 4; Length 526;
Best Local Similarity 99.0%; Pred. No. 1.2e-109;
Matches 489; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 28 GGGCGAAGAGTGGAGGAGGGGCGGTCCCGCGCGGTGGCGGTGCTATCGCTTCGAGAGA 87
DB 494 GGGCGAAGAGTGGAGGAGGGGCGGTCCCGCGCGGTGGCGGTGCTATCGCTTCGAGAGA 435
QY 88 ACCTACTCAGGCAAGCAGCTGAGAAAGTTGAGGAAAGTCTCTGCTGGCTGAGAGA 147
DB 434 ACCTACTCAGGCAAGCAGCTGAGAAAGTTGAGGAAAGTCTCTGCTGGCTGAGAGA 375
QY 148 CGCGATGATTAAGTGCAGCCGAAATTAACATC-GCCCTTCTGCTTCAGTGTGAAG 206
DB 374 CGCGATGATTAAGTGCAGCCGAAATTAACATC-GCCCTTCTGCTTCAGTGTGAAG 315
QY 207 GCCACGTGAAGATCTGGGCGGTGATTAATCACTGATGATTAACAGATTCATGCG 266
DB 314 GCCACGTGAAGATCTGGGCGGTGATTAATCACTGATGATTAACAGATTCATGCG 255
QY 267 TCATCTATCTGTGTGGCACTGATACAGAAACCAACAATTGACAGTTGGTGAAGGG 326
DB 254 TCATCTATCTGTGTGGCACTGATACAGAAACCAACAATTGACAGTTGGTGAAGGG 195
QY 327 TGTTCGACTTGACAGCAATGCTGTCTTCCGAGCGGGCCCTTATTTACCGGAAGC 386
DB 194 TGTTCGACTTGACAGCAATGCTGTCTTCCGAGCGGGCCCTTATTTACCGGAAGC 135
QY 387 TTTCGTCAATCCAGGCGTCTTACAGAAAGCCGTGCAAGAAAGAAAGTT 446
DB 134 TTTCGTCAATCCAGGCGTCTTACAGAAAGCCGTGCAAGAAAGAAAGTT 75
QY 447 TGTATTTATTAATCTTTTATTTAGTTGATACTAGTATTAACATATTTT-TGTATTTCTT 505
DB 74 TGTATTTATTAATCTTTTATTTAGTTGATACTAGTATTAACATATTTTGTATTTCTT 15
QY 506 CCAAAAAAAAAA 519
DB 14 CCAAAAAAAAAA 1

RESULT 6
US-09-663-600A-147
Sequence 147, Application US/09663600A
Patent No. 6573068
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleret, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: 31. US3.CIP
CURRENT APPLICATION NUMBER: US/09/663.600A
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: 09/191,997
PRIOR FILING DATE: 1998-11-13
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229

SOFTWARE: Patent.pm
SEQ ID NO 147
LENGTH: 413
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig.peptide
LOCATION: 46..189
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.0999990463257
OTHER INFORMATION: seq VFMILVSLALIE/ET
NAME/KEY: polyA_signal
LOCATION: 377..382
NAME/KEY: polyA_site
LOCATION: 402..413
US-09-663-600A-147

Query Match 77.0%; Score 411.4; DB 4; Length 413;
Best Local Similarity 99.8%; Pred. No. 7.7e-96;
Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 107 TGAGAGAGTTGAGGGAAGTGTGCTGCTGGGTGCAAGCCGATGATAAGTGCAG 166
DB 1 TGAGAGAGTTGAGGGAAGTGTGCTGCTGGGTGCAAGCCGATGATAAGTGCAG 60
QY 167 CCGAAATTAAGATCGCCCTTCTGCTTCAGTGTGAAGCCACGTGAAGATGCTCGG 226
DB 61 CCGAAATTAAGATCGCCCTTCTGCTTCAGTGTGAAGCCACGTGAAGATGCTCGG 120
QY 227 CTGATTTATTAACAATCACTGATTAACAAGATTTATGCTATCTGATCTGTTGGCA 286
DB 121 CTGATTTATTAACAATCACTGATTAACAAGATTTATGCTATCTGATCTGTTGGCA 180
QY 287 CTGATTAACAAGAACCAATTAAGATTAAGATTTATGCTATCTGATCTGTTGGCA 346
DB 181 CTGATTAACAAGAACCAATTAAGATTAAGATTTATGCTATCTGATCTGTTGGCA 240
QY 347 GATAGCTGTCTTCCGAGCGGGCCCTTATTTACCGAAGCTTCTGTTCAATCCAGCGGT 406
DB 241 GATAGCTGTCTTCCGAGCGGGCCCTTATTTACCGAAGCTTCTGTTCAATCCAGCGGT 300
QY 407 CTTACCAAGAAAGCCTGTGCATGAAAGAAAGAAAGTTGTATTTATTTATTTACTTTT 466
DB 301 CTTACCAAGAAAGCCTGTGCATGAAAGAAAGAAAGTTGTATTTATTTATTTACTTTT 360
QY 467 TAGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAA 519
DB 361 TAGTTGATTAAGTATTAACATATTTCTGATTTCTTCCAAAAA 413

RESULT 7
US-09-599-360B-70
Sequence 70, Application US/09599360B
Patent No. 6548633
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J. B.
APPLICANT: Bougueleret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: US/09/599.360B
PRIOR FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 70
LENGTH: 669
TYPE: DNA

EARLIER APPLICATION NUMBER: 60/048,880
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,020
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,876
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,895
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,884
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,894
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,882
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,899
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,893
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,900
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,901
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,892
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,915
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,373
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,875
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,374
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,949
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,883
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,898
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,877
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/094,657
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 64
LENGTH: 588
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (565)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (566)
OTHER INFORMATION: n equals a,t,g, or c
US-09-205-258-64

Query Match 8.4%; Score 44.6; DB 4; Length 588;
Best Local Similarity 71.1%; Pred. No. 0.024;
Matches 59; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 452 TTTTATATTACTTTTGTGTTGATTAAGTATTAAACATATTCTGTATCTTCAGAA 511
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Db 440 TTTTATTCCTGTGGGCTCACCCCAAGTATTAAAGTAGCTTGTATTCAGAA 499
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QY 512 AAAAAAAAAAAAAAAAAAAAAA 534
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Db 500 AAAAAAAAAAAAAAAAAAAAAA 522
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Search completed: January 31, 2004, 04:11:09
Job time : 79 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 31, 2004, 02:55:12 ; Search time 281 Seconds

(without alignments)
6925.954 Million cell updates/sec

Title: US-09-801-115B-1

Perfect score: 534

Sequence: 1 gtcccaatctgaagtcgaag.....aaaaaaaaaaaaa 534

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2434939 seqs, 1822278265 residues 4869878

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/1/pubpna/PCR_NEW_PUB.seq:*
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- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	534	100.0	534	9	US-09-801-115-1
2	509.4	95.4	817	13	US-10-119-428-14
3	507	94.9	655	15	US-10-291-172-13
4	497.2	93.1	558	15	US-10-106-698-1927
5	486.6	91.1	504	11	US-09-809-391-98
6	486.6	91.1	504	11	US-09-882-171-98
7	478.6	89.6	506	11	US-09-809-391-252
8	478.6	89.6	506	11	US-09-882-171-252
9	466.8	87.4	500	13	US-10-319-763-53
10	460.2	86.2	512	11	US-09-918-995-19489
11	425	79.6	439	11	US-09-822-846-397
12	411.4	77.0	413	13	US-10-319-763-147
13	404	75.7	422	11	US-09-918-995-6534
14	368.4	69.0	400	12	US-10-242-535A-7940
15	335	62.7	663	10	US-09-978-295A-189

16	335	62.7	663	10	US-09-978-697-189	Sequence 189, App
17	335	62.7	663	10	US-09-978-192A-189	Sequence 189, App
18	335	62.7	663	10	US-09-999-833A-189	Sequence 189, App
19	335	62.7	663	11	US-09-978-189-189	Sequence 189, App
20	335	62.7	663	11	US-09-978-608A-189	Sequence 189, App
21	335	62.7	663	11	US-09-978-568A-189	Sequence 189, App
22	335	62.7	663	11	US-09-978-191A-189	Sequence 189, App
23	335	62.7	663	11	US-09-978-403A-189	Sequence 189, App
24	335	62.7	663	11	US-09-978-564A-189	Sequence 189, App
25	335	62.7	663	11	US-09-999-833A-189	Sequence 189, App
26	335	62.7	663	11	US-09-981-915A-189	Sequence 189, App
27	335	62.7	663	11	US-09-978-824-189	Sequence 189, App
28	335	62.7	663	11	US-09-918-585A-189	Sequence 189, App
29	335	62.7	663	11	US-09-978-423A-189	Sequence 189, App
30	335	62.7	663	11	US-09-978-193A-189	Sequence 189, App
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32	335	62.7	663	11	US-09-978-757A-189	Sequence 189, App
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34	335	62.7	663	11	US-09-978-643A-189	Sequence 189, App
35	335	62.7	663	12	US-10-013-919A-189	Sequence 189, App
36	335	62.7	663	12	US-10-013-920A-189	Sequence 189, App
37	335	62.7	663	12	US-10-145-093A-189	Sequence 189, App
38	335	62.7	663	13	US-09-978-375A-189	Sequence 189, App
39	335	62.7	663	13	US-09-978-188A-189	Sequence 189, App
40	335	62.7	663	13	US-09-978-298A-189	Sequence 189, App
41	335	62.7	663	13	US-10-143-031A-189	Sequence 189, App
42	335	62.7	663	13	US-10-002-967A-189	Sequence 189, App
43	335	62.7	663	13	US-10-017-083A-189	Sequence 189, App
44	335	62.7	663	13	US-10-143-030A-189	Sequence 189, App
45	335	62.7	663	13	US-10-143-128A-189	Sequence 189, App

ALIGNMENTS

RESULT 1
US-09-801-115-1
Sequence 1, Application US/09801115
Patent No. US20020001828A1
GENERAL INFORMATION:
APPLICANT: Ma, D.
APPLICANT: Han, W.
APPLICANT: Zhang, Y.
APPLICANT: Song, Q.
APPLICANT: Di, C.
APPLICANT: Huang, J.
APPLICANT: Tang, J.
TITLE OF INVENTION: CHEMOKINE LIKE FACTOR (CKLF) WITH CHEMOTACTIC AND HEMATOPOIETIC
FILE REFERENCE: 10776-003-999
CURRENT APPLICATION NUMBER: US/09/801,115
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/CN00/00026
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 99107284.7
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 1
LENGTH: 534
TYPE: DNA
ORGANISM: Homo sapiens
US-09-801-115-1
Query Match 100.0%; Score 534; DB 9; Length 534;
Best local Similarity 100.0%; Pred. No. 8.7e+123;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTTCCCAATCTGAAGTGAAGCCGAGCGGCGAGAGTAGGGAGGCGGTGCTCCGCCG 60
DB 1 GTTCCCAATCTGAAGTGAAGCCGAGCGGCGAGAGTAGGGAGGCGGTGCTCCGCCG 60
QY 61 CGGTGCGGTGTTATCGCTTCCAGAACCTACTCAGGCGAGCGAGCTGAGAGAGTTGAG 120

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Db 61 CGGTGGCGGTGCTATCGCTTCGACAGAACTTACTCAGCGACCGAGCTGAGAAAGTTGAG 120
Qy 121 GGAAGTGTCTGTCTGGGCTCTGACAGAGCGATGATTAAGCCGAGAAATTAACA 180
Db 121 GGAAGTGTCTGTCTGGGCTCTGACAGAGCGATGATTAAGCCGAGAAATTAACA 180
Qy 181 TCGCCCTTCTGCTTCACTGATGAAAGGCGATGAAAGTGTGGCTGATATTATCAA 240
Db 181 TCGCCCTTCTGCTTCACTGATGAAAGGCGATGAAAGTGTGGCTGATATTATCAA 240
Qy 241 CTCCTGTGTAACAAGTATTCATGCTCATGTAATCTGTGGCAGTGAATCCAGAAAC 300
Db 241 CTCCTGTGTAACAAGTATTCATGCTCATGTAATCTGTGGCAGTGAATCCAGAAAC 300
Qy 301 CACAACATTCAGAGTTGGTGGAGGGGTGTTCGACCTTGTGACAGCAGATCTCTTGC 360
Db 301 CACAACATTCAGAGTTGGTGGAGGGGTGTTCGACCTTGTGACAGCAGATCTCTTGC 360
Qy 361 CGACGGGCGCTTATTTACCGGAAGCTTCTGTCAATCCAGCGCTCTTACAGAAAA 420
Db 361 CGACGGGCGCTTATTTACCGGAAGCTTCTGTCAATCCAGCGCTCTTACAGAAAA 420
Qy 421 GCCTGTGATGAAAAAAGAAAGTTTGTAAATTTATTTACTTTTGTGATCTAA 480
Db 421 GCCTGTGATGAAAAAAGAAAGTTTGTAAATTTATTTACTTTTGTGATCTAA 480
Qy 481 GTATTAAACATATTTCTGTATTTCTTCCAAAAAATTTTAAAAAATTTAAAAA 534
Db 481 GTATTAAACATATTTCTGTATTTCTTCCAAAAAATTTTAAAAAATTTAAAAA 534
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RESULT 2

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US-10-119-428-14
; Sequence 14, Application US/10119428
; Publication No. US20030165881A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Xu, Chongjun
; APPLICANT: Wehtman, Tom
; APPLICANT: Ren, Feiyan
; APPLICANT: Ma, Yundong
; APPLICANT: Zhou, Ping
; APPLICANT: Zhao, Qing A.
; APPLICANT: Yang, Yonghong
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030165881A1el Nucleic Acids and
; FILE REFERENCE: 789CIP2
; CURRENT APPLICATION NUMBER: US/10/119,428
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: pc_fl_genes version 1.0
; SEQ ID NO 14
; LENGTH: 817
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (236)..(535)
US-10-119-428-14
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Query Match 95.4%; Score 509.4; DB 13; Length 817;
Best Local Similarity 99.8%; Pred. No. 1.4e-116;
Matches 510; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 15 GTGAGCCGAGCTGGGCGAAGTAAGGAGGCGGTCTCCGCCGCGTGGCGTTGCT 74
Db 99 GGAAGCCGAGCTGGGCGAAGTAAGGAGGCGGTCTCCGCCGCGTGGCGTTGCT 158
Qy 75 ATGCTTCCGAGAACTTACTCAGGACGCCAGCTGAGAAAGTTGAGGAAAGTCTG 134
Db 159 ATGCTTCCGAGAACTTACTCAGGACGCCAGCTGAGAAAGTTGAGGAAAGTCTG 218
Qy 135 CTGGGTCTGAGACGCGATGATTAAGTGAAGCCGAGAAATTAACAATCGCCCTTCT 194
Db 219 CTGGGTCTGAGACGCGATGATTAAGTGAAGCCGAGAAATTAACAATCGCCCTTCT 278
Qy 195 TCAAGTGAAGGCGACGTAAGATGCTGGGCTGATATTATCACTCACTGTAACAA 254
Db 279 TCAAGTGAAGGCGACGTAAGATGCTGGGCTGATATTATCACTCACTGTAACAA 338
Qy 255 CAGTATTCATGCTCATGTAATCTGTGTGGCAGTGAATCCAGAAACCAAACTGAC 314
Db 339 CAGTATTCATGCTCATGTAATCTGTGTGGCAGTGAATCCAGAAACCAAACTGAC 398
Qy 315 TTGGTGAAGGGGTGTGTTGCACTTGTGACAGCAGTATGCTCTTGGCGAGCGGGCT 374
Db 399 TTGGTGAAGGGGTGTGTTGCACTTGTGACAGCAGTATGCTCTTGGCGAGCGGGCT 458
Qy 375 TTACCGGAAGCTTCTGTGTAATCCAGCGGCTTACAGAAAAAGCTGTGCATGAAA 434
Db 459 TTACCGGAAGCTTCTGTGTAATCCAGCGGCTTACAGAAAAAGCTGTGCATGAAA 518
Qy 435 AAAAAGAAAGTTTGTAAATTTTATTTACTTTTGTGATTTAAATTAACATATT 494
Db 519 AAAAAGAAAGTTTGTAAATTTTATTTACTTTTGTGATTTAAATTAACATATT 578
Qy 495 TCTGTATTTCTCCAAAAAATTTTAAAAAATTTAAAAA 525
Db 579 TCTGTATTTCTCCAAAAAATTTTAAAAAATTTAAAAA 609
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RESULT 3

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US-10-291-172-13
; Sequence 13, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/291,172
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 13
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (134)..(430)
US-10-291-172-13
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Query Match 94.9%; Score 507; DB 12; Length 655;
Best Local Similarity 100.0%; Pred. No. 5.1e-116;
Matches 507; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	19	AGCCGAGCTGGGGCCGAGAAGT	AGGGGAGGCGGCTCTCCGCGCGGTGACGGTTCTCTATTCG	78
Db	1	AGCCGAGCTGGGGCCGAGAAGT	AGGGGAGGCGGCTCTCCGCGCGGTGACGGTTCTCTATTCG	60
QY	79	CTTCGCAGAACTTACTACAGCGAGCCAGCTGAGAAAGTTGAGGAAAGTGTCTGTCTGG	138	
Db	61	CTTCGCAGAACTTACTACAGCGAGCCAGCTGAGAAAGTTGAGGAAAGTGTCTGTCTGG	120	
QY	139	GTCGTGACAGCGCGATGATATAACGTGCAGCCGAAAAATAAACATGCGCCCTTCTGCTTCAG	198	
Db	121	GTCGTGACAGCGCGATGATATAACGTGCAGCCGAAAAATAAACATGCGCCCTTCTGCTTCAG	180	
QY	199	TGTGAAAAGGCCACGTGAAGATGCTGCGGCTGTGATATTTCACTCACTGTGTAACAAACGT	258	
Db	181	TGTGAAAAGGCCACGTGAAGATGCTGCGGCTGTGATATTTCACTCACTGTGTAACAAACGT	240	
QY	259	ATTGATGTCTATCGATCTGTGTTGGCACTGATACCGAAAACCAACAATTCAGAGTTGG	318	
Db	241	ATTGATGTCTATCGATCTGTGTTGGCACTGATACCGAAAACCAACAATTCAGAGTTGG	300	
QY	319	TGAGAGGGGTGTTTSCACTTGTGACAGCAGTATGTGTCCTTTCGACGAGGGGCCCTTATTTTA	378	
Db	301	TGAGAGGGGTGTTTSCACTTGTGACAGCAGTATGTGTCCTTTCGACGAGGGGCCCTTATTTTA	360	
QY	379	CCGGAAGCTTCGTTCAAATCCACAGCGGTCTTACCCAGAAAAAGCCCTGTGCATGAAAAAA	438	
Db	361	CCGGAAGCTTCGTTCAAATCCACAGCGGTCTTACCCAGAAAAAGCCCTGTGCATGAAAAAA	420	
QY	439	AGAAATTGTAATTTTATTTATTTACTTTTAACTTGTGATCTAAAGTATTTAAACATATTTCTG	498	
Db	421	AGAAATTGTAATTTTATTTATTTACTTTTAACTTGTGATCTAAAGTATTTAAACATATTTCTG	480	
QY	499	TATTCCTTCCAAAAAATTTTTTTTTTTT	525	
Db	481	TATTCCTTCCAAAAAATTTTTTTTTTTT	507	

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RESULT 4
US-10-106-698-1927
; Sequence 1927, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION: 1
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides
; FILE REFERENCE: PAO0501
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 1927
; LENGTH: 558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (514)..(514)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-1927

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	Query Match	Similarity	Score	497.2	DB 15	Length	558	
	Best Local	Similarity	98.4%	Pred	No. 1.3e-113			
	Matches	499	Conservative	2	Mismatches	6	Indels	0
								Gaps
								0
Qy	16	TGAACCCGAGCTGGCGGAGAGTATAGCGGAGGGCGGTCTCCGCCGCGGTGGCGGTTTGCTA						75
	:	:						
	:	:						
Db	11	TGAACGAGGAGCTGGCGGAGAGTATAGCGGAGGGCGGTCTCCGCCGCGGTGGCGGTTTGCTA						70

Qy	136	TGGGTCGACAGCGGATGATTAACGTGACGCCGAAATATAAACATCGGCCCTTCGCTT	195
Db	131	TGGGTCGACAGCGGATGATTAACGTGACGCCGAAATATAAACATCGGCCCTTCGCTT	190
Qy	196	CAGTGTGAAGGCCACGTGAAAGATGCTGCGGCTGGATATATATCACTCACTGGTAACAAC	255
Db	191	CAGTGTGAAGGCCACGTGAAAGATGCTGCGGCTGGATATATATCACTCACTGGTAACAAC	250
Qy	256	AGTATTCACTCATCGATCTGATGTTGGCACTGATACCAAAACCAACAATGACAGT	315
Db	251	AGTATTCACTCATCGATCTGATGTTGGCACTGATACCAAAACCAACAATGACAGT	310
Qy	316	TGGTGAAGGGGCTTTGCACTTGTGACAGCAGTATGCTGTCTTGGCGAAGGGGCCCTTAT	375
Db	311	TGGTGAAGGGGCTTTGCACTTGTGACAGCAGTATGCTGTCTTGGCGAAGGGGCCCTTAT	370
Qy	376	TTACCGGAAGCTTCTGTTCAATCCACGAGGTCCTTACCAAGAAAAGCCTGTGCATGAAA	435
Db	371	TTACCGGAAGCTTCTGTTCAATCCACGAGGTCCTTACCAAGAAAAGCCTGTGCATGAAA	430
Qy	436	AAAAGAAAGTTTGTATTTTATATATTTACTTTTAACTTGTGATPCTPAATATTAATTT	495
Db	431	AAAAGAAAGTTTGTATTTTATATATTTACTTTTAACTTGTGATPCTPAATATTAATTT	490
Qy	496	CTGTATCTTCCAAAAAATTTTTTTTTT	522
Db	491	CTGTATCTTCCAAAAAATTTTTTTTTT	517

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RESULT 5
US-09-809-391-98
; Sequence 98, Application US/09809391
; Publication No. US20030049618A1
GENERAL INFORMATION:
; APPLICANT: Ruden et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-809-391-98

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Query Match	91.1%	Score 486.6	DB 11	Length 504
Best Local Similarity	99.0%	Pred. No. 5.2e-111		
Matches 500	Conservative 0	Mismatches 4	Indels 1	Gaps 1
Qy	21	CCGAGCTGGGCGAAGTAGGGGAGGCGGTCTCCGCCGCGGTGCGGTTCATATCGT	80	
Db	1	CCGAGCTGGGCGAAGTAGGGGAGGCGG-ACGAGCCCGCGGTGCGGTTCATATCGCT	59	
Qy	81	TCCGCAACCTACTCAGGCGAGCCAGCTAGAGAGTTGAGGGAAAGTGCCTGCTGGGT	140	
Db	60	TCCGCAACCTACTCAGGCGAGCCAGCTAGAGAGTTGAGGGAAAGTGCCTGCTGGGT	119	
Qy	141	CTGCAGACGCGATGAGTAACTGTCAGCCGAAATATAAATCATGCCCTTCTGCTTCAGTG	200	
Db	120	CTGCAGACGCGATGAGTAACTGTCAGCCGAAATATAAATCATGCCCTTCTGCTTCAGTG	179	
Qy	201	TGAAAGGCCACGTGAAGATGCTGCGGCTGAGTATTATCAATCATCTGAGTAAACAACGTAT	260	
Db	180	TGAAAGGCCACGTGAAGATGCTGCGGCTGAGTATTATCAATCATCTGAGTAAACAACGTAT	239	

Qy 261 TCATGCTCATGTAATCTGTGTGGCACTGATACCAAGAACCAACATGACAGTTGGTG 320
Db 240 TCATGCTCATGTAATCTGTGTGGCACTGATACCAAGAACCAACATGACAGTTGGTG 299
Qy 321 GAGGGGTGTGGCACTGTGACAGAGATGCTGTGGAGGGGGCCCTTATTTTACC 380
Db 300 GAGGGGTGTGGCACTGTGACAGAGATGCTGTGGAGGGGGCCCTTATTTTACC 359
Qy 381 GGAAGCTTGTGTAATCCAGCGGTCTTACCAAGAAAGCCTGTGATGAAAAAAG 440
Db 360 GGAAGCTTGTGTAATCCAGCGGTCTTACCAAGAAAGCCTGTGATGAAAAAAG 419
Qy 441 AAGTTTGTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 500
Db 420 AAGTTTGTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 479
Qy 501 TTCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 525
Db 480 TTCTTCCAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 504

RESULT 6
US-09-882-171-98

Sequence 98, Application US/09882171
Publication No. US20030175858A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002P2
CURRENT APPLICATION NUMBER: US/09/882,171
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 09/809,391
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
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; PRIOR APPLICATION NUMBER: 60/056,884
 ; PRIOR FILING DATE: 1997-08-22
 ; PRIOR APPLICATION NUMBER: 60/057,669
 ; PRIOR FILING DATE: 1997-09-05

Query Match 91.1%; Score 486.6; DB 13; Length 504;
 Best Local Similarity 99.0%; Pred. No. 5.2e-111;
 Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 21 CCGAGCTGGCGAGAGTAGAGGAGGCGGTGCTCCGCGCGGTGGCGGTGCTATCGCT 80
 DB 1 CCGAGCTGGCGAGAGTAGAGGAGGCGGTGCTCCGCGCGGTGGCGGTGCTATCGCT 59
 QY 81 TCGCAGAACCTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGT 140
 DB 60 TCGCAGAACCTACTCAGGCGAGCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGGT 119
 QY 141 CTGCAAGCGGAGAGTAGAGTAGAGTACCGGAGAAATTAATCGCCCTTGTGCTTCAAGT 200
 DB 120 CTGCAAGCGGAGAGTAGAGTAGAGTACCGGAGAAATTAATCGCCCTTGTGCTTCAAGT 179
 QY 201 TGAAGGCCACGTGAAGATGCTCGGCTGGATATTTCAACTGACTGTGTAACAAGTAT 260
 DB 180 TGAAGGCCACGTGAAGATGCTCGGCTGGATATTTCAACTGACTGTGTAACAAGTAT 239
 QY 261 TCATGCTCATCGATCTGATGTTGGCACTGATACAGAAACCAACAATTGACAGTTGGT 320
 DB 240 TCATGCTCATCGATCTGATGTTGGCACTGATACAGAAACCAACAATTGACAGTTGGT 299
 QY 321 GAGGGGTGTTGGCACTTGTGACAGCGATGCTGCTCTGGCGAGCGGGCCCTTATTTACC 380
 DB 300 GAGGGGTGTTGGCACTTGTGACAGCGATGCTGCTCTGGCGAGCGGGCCCTTATTTACC 359
 QY 381 GGAAGCTTCTGTCATATCCAGCGGCTCTTACCAAGAAAGCCTGTGATGAAAGAAAG 440
 DB 360 GGAAGCTTCTGTCATATCCAGCGGCTCTTACCAAGAAAGCCTGTGATGAAAGAAAG 419
 QY 441 AAGTTTGTATTTATTTATTTATTTAGTTGATGATTAAGTATTAACATATTTCTGTA 500
 DB 420 AAGTTTGTATTTATTTATTTATTTAGTTGATGATTAAGTATTAACATATTTCTGTA 479
 QY 501 TTCTTCCAAAAAAGAAAAA 525
 DB 480 TTCTTCCAAAAAAGAAAAA 504

RESULT 7
 US-09-809-391-252
 ; Sequence 252, Application US/09809391
 ; Publication No. US20030049618A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: 186 Human Secreted proteins
 ; FILE REFERENCE: P2002P2
 ; CURRENT APPLICATION NUMBER: US/09/809,391
 ; CURRENT FILING DATE: 2001-03-16
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 761
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 252
 ; LENGTH: 506
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-809-391-252

Query Match 89.4%; Score 478.6; DB 11; Length 506;
 Best Local Similarity 97.4%; Pred. No. 5.1e-109;
 Matches 484; Conservative 2; Mismatches 11; Indels 0; Gaps 0;
 QY 37 GTAGGGAGGCGGTGCTCCGCGCGGTGGCGGTGCTATCGCTTGGCAGAACTTACTCA 96
 DB 2 GAGGATTTGGCAGGACCCCGCGGTGGCGGTGCTATCGCTTGGCAGAACTTACTCA 61

QY 97 GGCAGCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGTCTGACGACGGGATGGA 156
Db 62 GGCAGCCAGCTGAGAGAGTTGAGGAGAAAGTCTGCTGGTCTGACGACGGGATGGA 121
QY 157 TAACGTGAGCCGAAATTAATCAATCCGCCCTTCTGCTTCAAGTGGAAAGCCACGCGAA 216
Db 122 TAACGTGAGCCGAAATTAATCAATCCGCCCTTCTGCTTCAAGTGGAAAGCCACGCGAA 181
QY 217 GATGCTGGGCTGATATTAATCAACTCACTGGTAACAACAGTATTCATGCTCATGATTC 276
Db 182 GATGCTGGGCTGATATTAATCAACTCACTGGTAACAACAGTATTCATGCTCATGATTC 241
QY 277 TGTGTGGCACTGATATCAAGAAACCAACATGACAGTTGGTGGAGGGGTGTTGCACT 336
Db 242 TGTGTGGCACTGATATCAAGAAACCAACATGACAGTTGGTGGAGGGGTGTTGCACT 301
QY 337 TGTGACAGCATATCTCTTCTTCCGACGGGCGCTTTATTAACGGAGCTTCGTTCAA 396
Db 302 TGTGACAGCATATCTCTTCTTCCGACGGGCGCTTTATTAACGGAGCTTCGTTCAA 361
QY 397 TCCGAGCGCTCTTACAGAAAGAAAGCTGTGATGAAAGAAAGAGTTTGTATTTTA 456
Db 362 TCCGAGCGCTCTTACAGAAAGAAAGCTGTGATGAAAGAAAGAGTTTGTATTTTA 421
QY 457 TATTACTTTTATGTTTACTACTAGTATTAACATATTTCTGTATTTCTTCCAAAAAAA 516
Db 422 TATTACTTTTATGTTTACTACTAGTATTAACATATTTCTGTATTTCTTCCAAAAAAA 481
QY 517 AAAAAAAAAAAAAA 533
Db 482 AAAAAAAAAAAAAA 498

RESULT 8

US-09-882-171-252
; Sequence 252, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
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Query Match	89.6%;	Score 478.6;	DB 13;	Length 506;
Best Local Similarity	97.4%;	Pred. No. 5.1e-109;		
Matches 484;	Conservative 2;	Mismatches 11;	Indels 0;	Gaps 0;

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OY      37 GTGAGGGGAAGGGGGTGTCCGCGCGGGGGGGTGGCTATCGCTCCAGAACTTACTCA   96
Db      2 GCAGGATTTGGCCAGAGACCCGCCGGGGGGGTTGCTATCGCTTCCGAACTTACTCA   61
OY      97 GGCAGCGACCTAGAGAAGATTGAGGGAAAGTGCTGCTCTGGGTCTGCAGACGGATGGA   156
Db      62 GCGAGCGACCTAGAGAAGATTGAGGGAAAGTGCTGCTGCTGGTCTGCAGACGGATGGA   121
OY      157 TAACTGTCAGCCGAAATMAAACATGCCCCCTTCTGCTTCAGTGTAAAGGCCACGTGAA   216
Db      122 TAACTGTCAGCCGAAATMAAACATGCCCCCTTCTGCTTCAGTGTGAAAGGCCACGTGAA   181
OY      217 GAGCTCGCGGCTGGATATTATTAATCACTGCTGTAAACAAGATATTCAATGCTCATCGTATC   278
Db      182 GAGCTCGCGGCTGGATATTATTAATCACTGCTGTAAACAAGATATTCAATGCTCATCGTATC   241
OY      277 TGTGTTGGCACTGATATCCAGAAACACAAACATTGACAGTTGGTGGAGGGGTTTGGACT   336
Db      242 TGTGTTGGCACTGATATCCAGAAACACAAACATTGACAGTTGGTGGAGGGGTTTGGACT   301
OY      337 TGTGACAGAGTATGTGCTGTCCGACGAGGGGCCCTTATTTACCGGAAGCTTCTGTTCAA   398
Db      302 TGTGACAGAGTATGTGCTGTCCGACGAGGGGCCCTTATTTACCGGAAGCTTCTGTTCAA   361
OY      397 TCCGACGCGTCTTATCCAGAAAAAGCTGTGCATGAAAAAAGAGTTTGTGATTTTA   456
Db      362 TCCGACGCGTCTTATCCAGAAAAAGCTGTGCATGAAAAAAGAGTTTGTGATTTTA   421
OY      457 TATTACTTTTGTGTTGATCTTAAGTATTTAAACATATTTCTGTATTTCTTCCAAAAAAA   516
Db      422 TATTACTTTTGTGTTGATCTTAAGTATTTAAACATATTTCTGTATTTCTTCCAAAAAAA   481
OY      517 AAAAAAAAAAAAAAAAAA 533
Db      482 AAAAAAAAAAAAAAAAAA 498

RESULT 9
US-10-319-763-53
; Sequence 53, Application US/10319763
; Publication No. US20030144490A1
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OR INVENTION: EXTENDED CDNAs FOR SECRETED PROTEINS
; FILE REFERENCE: G-031.US04.DIV
; CURRENT APPLICATION NUMBER: US/10/319,763
; CURRENT FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957

```

PRIOR FILING DATE: 1997-12-17	OTHER INFORMATION: id :W93646
PRIOR APPLICATION NUMBER: 60/074,121	OTHER INFORMATION: est
PRIOR FILING DATE: 1998-02-09	FEATURE:
PRIOR FILING DATE: 1998-02-09	NAME/KEY: misc_feature
PRIOR APPLICATION NUMBER: 60/081,563	LOCATION: 425..488
PRIOR FILING DATE: 1998-04-13	OTHER INFORMATION: misc_feature
PRIOR APPLICATION NUMBER: 60/096,116	OTHER INFORMATION: id :W93646
PRIOR FILING DATE: 1998-08-10	OTHER INFORMATION: est
PRIOR APPLICATION NUMBER: 60/099,273	FEATURE:
PRIOR FILING DATE: 1998-09-04	NAME/KEY: misc_feature
NUMBER OF SEQ ID NOS: 229	LOCATION: 197..412
SOFTWARE: Patent..pm	OTHER INFORMATION: misc_feature
SEQ ID NO 53	OTHER INFORMATION: id :AA5164311
LENGTH: 500	OTHER INFORMATION: est
TYPE: DNA	FEATURE:
ORGANISM: Homo sapiens	NAME/KEY: misc_feature
FEATURE:	LOCATION: 90..195
NAME/KEY: sig_peptide	OTHER INFORMATION: misc_feature
LOCATION: 199..288	OTHER INFORMATION: id :AA5164311
OTHER INFORMATION: Von Heijne matrix	OTHER INFORMATION: est
OTHER INFORMATION: score 5.599999990463257	FEATURE:
OTHER INFORMATION: seq IVSVALIPETTY/LT	NAME/KEY: misc_feature
FEATURE:	LOCATION: 425..488
NAME/KEY: polyA_signal	OTHER INFORMATION: misc_feature
LOCATION: 464..469	OTHER INFORMATION: id :AA5164311
FEATURE:	OTHER INFORMATION: est
NAME/KEY: polyA_site	FEATURE:
LOCATION: 489..500	NAME/KEY: misc_feature
FEATURE:	LOCATION: 52..195
NAME/KEY: misc_feature	OTHER INFORMATION: misc_feature
LOCATION: 197..412	OTHER INFORMATION: id :W38899
OTHER INFORMATION: misc_feature	OTHER INFORMATION: est
OTHER INFORMATION: id :AA429945	FEATURE:
OTHER INFORMATION: est	NAME/KEY: misc_feature
FEATURE:	LOCATION: 197..324
NAME/KEY: misc_feature	OTHER INFORMATION: misc_feature
LOCATION: 61..195	OTHER INFORMATION: id :W38899
OTHER INFORMATION: misc_feature	OTHER INFORMATION: est
OTHER INFORMATION: id :AA429945	FEATURE:
OTHER INFORMATION: est	NAME/KEY: misc_feature
FEATURE:	LOCATION: 197..338
NAME/KEY: misc_feature	OTHER INFORMATION: misc_feature
LOCATION: 197..412	OTHER INFORMATION: id :W52820
OTHER INFORMATION: misc_feature	OTHER INFORMATION: est
OTHER INFORMATION: id :AA455042	FEATURE:
OTHER INFORMATION: est	NAME/KEY: misc_feature
FEATURE:	LOCATION: 71..195
NAME/KEY: misc_feature	OTHER INFORMATION: misc_feature
LOCATION: 61..195	OTHER INFORMATION: id :W52820
OTHER INFORMATION: misc_feature	OTHER INFORMATION: est
OTHER INFORMATION: id :AA455042	FEATURE:
OTHER INFORMATION: est	NAME/KEY: misc_feature
FEATURE:	LOCATION: 339..401
NAME/KEY: misc_feature	OTHER INFORMATION: misc_feature
LOCATION: 425..488	OTHER INFORMATION: id :W52820
OTHER INFORMATION: misc_feature	OTHER INFORMATION: est
OTHER INFORMATION: id :AA455042	FEATURE:
OTHER INFORMATION: est	NAME/KEY: misc_feature
FEATURE:	LOCATION: 425..469
NAME/KEY: misc_feature	OTHER INFORMATION: misc_feature
LOCATION: 207..412	OTHER INFORMATION: id :W52820
OTHER INFORMATION: misc_feature	OTHER INFORMATION: est
OTHER INFORMATION: id :W93646	FEATURE:
OTHER INFORMATION: est	NAME/KEY: misc_feature
FEATURE:	LOCATION: 40..195
NAME/KEY: misc_feature	OTHER INFORMATION: misc_feature
LOCATION: 58..195	OTHER INFORMATION: id :W19506
OTHER INFORMATION: misc_feature	
OTHER INFORMATION: homology	

US-09-822-846-397

Query Match 79.6%; Score 425; DB 11; Length 439;

Best Local Similarity 99.8%; Pred. No. 1e-95; Mismatches 0; Indels 1; Gaps 1;

Matches 436; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```
OY 72 GCTATCGCTTCGACAACTTCTCAGGAGCCAGCTGAGAAAGTTGGAGAAAGTGTG 131
DB 1 GCTATCGCTTCGACAACTTCTCAGGAGCCAGCTGAGAAAGTTGGAGAAAGTGTG 60
OY 132 CTGCTGGGTCTGCAGACCGCATGATTAAGTCGACCCGAAATTAAGATGCGCTTCT 191
DB 61 CTGCTGGGTCTGCAGACCGCATGATTAAGTCGACCCGAAATTAAGATGCGCTTCT 120
OY 192 GCTTCAGTGTGAAGGACGACGTAAGATGCTGGCTGGATTTATTTCACTGATTA 251
DB 121 GCTTCAGTGTGAAGGACGACGTAAGATGCTGGCTGGATTTATTTCACTGATTA 180
OY 252 CAACAGTATTCATGCTCATCTGATCTGTGTCAGTATACAGAAACCAACATTGA 311
DB 181 CAACAGTATTCATGCTCATCTGATCTGTGTCAGTATACAGAAACCAACATTGA 240
OY 312 CAGTTGGTGAAGGGGTGTTGCACTTGTGACAGCATATGCTGTTCGCCAGCGGGCC 371
DB 241 CAGTTGGTGAAGGGGTGTTGCACTTGTGACAGCATATGCTGTTCGCCAGCGGGCC 300
OY 372 TTATTTACCGAAGCTTCTGTTCAATCCAGCGGCTTACCGAAGAAAGCTGTGATG 431
DB 301 TTATTTACCGAAGCTTCTGTTCAATCCAGCGGCTTACCGAAGAAAGCTGTGATG 360
OY 432 AAAAAAAGAAAGTTTGTATTTTATTTATTTTATTTTATTTTATTTTATTTTATTT 490
DB 361 AAAAAAAGAAAGTTTGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 420
OY 491 TATTTCTGATTTCTTCC 507
DB 421 TATTTCTGATTTCTTCC 437
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RESULT 12

US-10-319-763-147

Sequence 147, Application US/10319763

Publication No. US20030144490A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Bouguerele, Lydie

TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: G-031.US04.DIV

CURRENT APPLICATION NUMBER: US/10/319,763

CURRENT FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/069,957

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/074,121

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/081,563

PRIOR FILING DATE: 1998-04-13

PRIOR APPLICATION NUMBER: 60/096,116

PRIOR FILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: 60/099,273

PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 229

SOFTWARE: Patent.pm

SEQ ID NO 147

LENGTH: 413

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: NAME/KEY: sig_peptide

LOCATION: 46..189

OTHER INFORMATION: Von Heijne matrix

OTHER INFORMATION: score 4.09999990463257

OTHER INFORMATION: seq VFMLIVSLALIP/ET

FEATURE: NAME/KEY: polyA signal

LOCATION: 377..382

FEATURE: NAME/KEY: polyA site

LOCATION: 402..413

US-10-319-763-147

Query Match 77.0%; Score 411.4; DB 13; Length 413;

Best Local Similarity 99.8%; Pred. No. 2.4e-92; Mismatches 1; Indels 0; Gaps 0;

Matches 412; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 107 TGAAGAGTGAAGGAAAGTGTGCTGCTGGGTCTGACAGCGGATGATTAAGTGCAG 166
DB 1 TGAAGAGTGAAGGAAAGTGTGCTGCTGGGTCTGACAGCGGATGATTAAGTGCAG 60
OY 167 CCGAAATTAACAATCGCCCTTCTGCTTCACTGTGAAGGCCACGTGAAGATGCTCGG 226
DB 61 CCGAAATTAACAATCGCCCTTCTGCTTCACTGTGAAGGCCACGTGAAGATGCTCGG 120
OY 227 CTGATTTTATTCATCTCATCTGTAACAAGATTTCAATGCTCATGCTGTGTTGCA 286
DB 121 CTGATTTTATTCATCTCATCTGTAACAAGATTTCAATGCTCATGCTGTGTTGCA 180
OY 287 CTGATTCAGAAACCAACAATGTAACAGTTGTGTGAAGGGTGTGTCATTTGACACA 346
DB 181 CTGATTCAGAAACCAACAATGTAACAGTTGTGTGAAGGGTGTGTCATTTGACACA 240
OY 347 GTATGCTGCTTGGCGAAGGGGCTTATTTTACCGAAGCTTCTGTTCAATCCAGGGT 406
DB 241 GTATGCTGCTTGGCGAAGGGGCTTATTTTACCGAAGCTTCTGTTCAATCCAGGGT 300
OY 407 CCTACAGAAAAAGCCTGTGCAATGAAGAAAAAGAGTTTGTATTTTATTTACTTTT 466
DB 301 CCTACAGAAAAAGCCTGTGCAATGAAGAAAAAGAGTTTGTATTTTATTTACTTTT 360
OY 467 TAGTTGATCTAAGTATTAACATATTTCTGATTTCTTCACAAAAAATTAATTTT 519
DB 361 TAGTTGATCTAAGTATTAACATATTTCTGATTTCTTCACAAAAAATTAATTTT 413
```

RESULT 13

US-09-918-995-6534

Sequence 6534, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054

SOFTWARE: PasteSeq for Windows Version 3.0

SEQ ID NO 6534

LENGTH: 422

TYPE: DNA

ORGANISM: Homo sapiens

US-09-918-995-6534

Query Match 75.7%; Score 404; DB 11; Length 422;

Best Local Similarity 100.0%; Pred. No. 1.7e-90; Mismatches 0; Indels 0; Gaps 0;

Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 122 GAAAGTGTGCTGTGCTGTCGACAGCGCATGATTAACGTGACCGGAAATTAACAT 181
DB 1 GAAAGTGTGCTGTGCTGTGTCGACAGCGCATGATTAACGTGACCGGAAATTAACAT 60
OY 182 CGCCCTTCTGCTTCACTGTGAAGGCGACGTGAAGATGCTGCGGTGATTTATCAAC 241
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Db 61 CGCCCTTCCTGCTCACTGTAAGAGCCAGTGAAGATGCTGGCGGCTGAGTATTATCAAC 120
Qy 242 TCACTGTAAACAAGATTTATCATGCTATCTGTGTGGCACTGATACAGAAACC 301
Db 121 TCACTGTAAACAAGATTTATCATGCTATCTGTGTGGCACTGATACAGAAACC 180
Qy 302 ACAACATTTGACAGTTGGTGAAGGGGTGTTGCACTTGTGACAGAGTATGCTGTGCC 361
Db 181 ACAACATTTGACAGTTGGTGAAGGGGTGTTGCACTTGTGACAGAGTATGCTGTGCC 240
Qy 362 GACGGGGCCCTTATTTCACCGAAGCTTGTGTAATCCGCGCTCTTACCGAAGAAAG 421
Db 241 GACGGGGCCCTTATTTCACCGAAGCTTGTGTAATCCGCGCTCTTACCGAAGAAAG 300
Qy 422 CCTGTGATGAAAAAAGAAAGTTTGTAAATTTATTAATTTTGTGTTGATTAAG 481
Db 301 CCTGTGATGAAAAAAGAAAGTTTGTAAATTTATTAATTTTGTGTTGATTAAG 360
Qy 482 TATTAAACATATTTCTGTATTTCTTCCAAAAAAGAAAAAAG 525
Db 361 TATTAAACATATTTCTGTATTTCTTCCAAAAAAGAAAAAAG 404

RESULT 14
US-10-242-535A-7940
Sequence 7940, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7940
LENGTH: 400
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
LOCATION: (176)..(176)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-7940

Query Match 69.0%; Score 368.4; DB 12; Length 400;
Best Local Similarity 99.2%; Pred. No. 1,2e-81;
Matches 380; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 55 CCGCGCGGTGGCGGTTGCTATGCTTCGAGAACTTACTAGGACCCAGCTGAGAA 114
Db 18 CCGCGCGGTGGCGGTTGCTATGCTTCGAGAACTTACTAGGACCCAGCTGAGAA 77
Qy 115 GTTGAAGGAAGTCTGCTGCTGCTGCAAGAGCGCATGATTAAGTGCAGCCGAAAT 174
Db 78 GTTGAAGGAAGTCTGCTGCTGCTGCAAGAGCGCATGATTAAGTGCAGCCGAAAT 137
Qy 175 AAAACATGCCCCCTTCTGCTTCACTGTGAAGGCAAGTGAAGTGTGCGGCTGATAT 234
Db 138 AAAACATGCCCCCTTCTGCTTCACTGTGAAGGCAAGTGAAGTGTGCGGCTGATAT 197
Qy 235 TATCACTCACTGTGAACAAGATTTCAATGCTCATGCTATCTGTGTTGCACTGATACC 294

Db 198 TATCACTCACTGTGTAAACAAGATTTATCATGCTCATGCTATCTGTGTGGCACTGATACC 257
Qy 295 AGAACAACAACATTTGACAGTTGTGGAGGGGTGTTGCA-CTTGTGACAGCATATGCT 353
Db 258 AGAACAACAACATTTGACAGTTGTGGAGGGGTGTTGCACTTGTGACAGCATATGCT 317
Qy 354 GTCTTGGCAGCGGGCCCTTATTATCCGGAAGCTTCTGTTCAATCCAGCGGTCTTACC 413
Db 318 GTCTTGGCAGCGGGCCCTTATTATCCGGAAGCTTCTGTTCAATCCAGCGGTCTTACC 377
Qy 414 AGAAAAAGCCTGTGCATGAAAAA 436
Db 378 AGAAAAAGCCTGTGCATGAAAAA 400

RESULT 15
US-09-978-295A-189
Sequence 189, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Denoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Nadier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004

Best Local Similarity 76.0%; Pred. No. 3.2e-73;
Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;

QY	22	CGAGCTGGGCGAAGATAGAGGAGGCGGTGTCTCCGCGCGGCGGATGCTATCGCTT	81
Db	1	CGAGCTGGGCGAAGATAGAGGAGGCGGTGTCTCCGCGCGGCGGATGCTATCGCTT	60
QY	82	CGCAGAACCTACTCAGCGACGACGCTGAGAAAGTTGAGGAAAGTCTGCTGTGGTTC	141
Db	61	CGCAGAACCTACTCAGCGACGACGCTGAGAAAGTTGAGGAAAGTCTGCTGTGGTTC	120
QY	142	TGCAGACCGGATGATATACGTGAGCCGAAATATAAATCATGTGCCCTTCTGCTTCACTGT	201
Db	121	TGCAGACCGGATGATATACGTGAGCCGAAATATAAATCATGTGCCCTTCTGCTTCACTGT	180
QY	202	GAAGGCGCACGTGAAGATCTGCGGCTG-----	229
Db	181	GAAGGCGCACGTGAAGATCTGCGGCTGCACTATACATCTATGACCTTTTAT	240
QY	230	-----	229
Db	241	CATCGCACAGCCCTGAAACCATATATTTGTATCATCAGATTGGAAGTACACCGTATCTT	300
QY	230	-----	229
Db	301	ATTTTCATCTTTTATATATGTACTCAGACTTGATGATTAATGAAGTATATTTGGCC	360
QY	230	-----	229
Db	361	TTTCTGTTGATTTATATCACTCACTGGTAAACAACATATTTCACTGCTATCTGTGT	420
QY	283	GGCACTGATACAGAAACCAACAACATGACAGTTGGTGGAGGGGTTTGACCTGTGAC	342
Db	421	GGCACTGATACAGAAACCAACAACATGACAGTTGGTGGAGGGGTTTGACCTGTGAC	480
QY	343	AGCAGTATGCTGTCTTGCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCATCCGAC	402
Db	481	AGCAGTATGCTGTCTTGCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCATCCGAC	540
QY	403	CGGTCTTATACAGAAAAAGCTGTGATGAAAAAAGAGTTTGTATTTATTTATAC	462
Db	541	CGGTCTTATACAGAAAAAGCTGTGATGAAAAAAGAGTTTGTATTTATTTATAC	600
QY	463	TTTTTATGTTGATATCAATGATTTAAACATATTTCTGTATTTCTTCCAAAAA	522
Db	601	TTTTTATGTTGATATCAATGATTTAAACATATTTCTGTATTTCTTCCAAAAA	660
QY	523	AAA 525	
Db	661	AAA 663	

Search completed: January 31, 2004, 04:16:04
Job time : 284 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2004, 03:35:03 ; Search time 1818 Seconds

(without alignments)
2227.752 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508
Sequence: 1 MDVNPQKIKRPFCSYKGH.....LFPNSGPYQKKPYHEKKEVL 99

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cg21/USFTO.spool_p/US09801115/runat.30012004.113848.7025/app_query.fasta.1.263
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=spct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US09801115.@CGN.1.1.4558.@runat.30012004.113848.7025 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

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2: gb_hcg.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vl.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
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25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*

29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rtd.*
36: em_htg_man.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htg_hum.*
40: em_htg_mus.*
41: em_htg_other.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	508	100.0	413	6 BD085952	BD085952 Elongatio
2	508	100.0	515	6 AR306550	AR306550 Sequence
3	508	100.0	515	6 AX061624	AX061624 Sequence
4	508	100.0	530	9 AF096895	AF096895 Homo sapi
5	491	96.7	526	6 AR275027	AR275027 Sequence
6	489	96.3	500	6 BD085905	BD085905 Elongatio
7	471.5	92.8	655	9 AF057306	AF057306 Homo sapi
8	471.5	92.8	669	6 AR306591	AR306591 Sequence
9	471.5	92.8	669	6 AX061665	AX061665 Sequence
10	471.5	92.8	688	9 BC004380	BC004380 Homo sapi
11	471.5	92.8	689	9 AF135380	AF135380 Homo sapi
12	461	90.7	415	6 BD023892	BD023892 Sequence
13	366	72.0	485	11 G30204	G30204 human STS S
14	339.5	66.8	593	9 AF145216	AF145216 Homo sapi
15	331	65.2	434	9 AF135381	AF135381 Homo sapi
16	323	63.6	321	6 BD139357	BD139357 Extended
17	318.5	62.7	495	6 AX079435	AX079435 Sequence
18	275	54.1	523	10 AF253064	AF253064 Rattus no
19	245	48.2	207	6 AX330610	AX330610 Sequence
20	245	48.2	207	6 AX330787	AX330787 Sequence
21	245	48.2	207	6 AX331008	AX331008 Sequence
22	245	48.2	207	6 AX408097	AX408097 Sequence
23	238.5	46.9	682	10 AF253065	AF253065 Rattus no
24	227.5	44.8	568	10 AY047360	AY047360 Mus muscu
25	215	42.3	151620	2 AC018589	AC018589 Homo sapi
26	215	42.3	180702	9 AC018557	AC018557 Homo sapi
27	215	42.3	188460	9 AC010542	AC010542 Homo sapi
28	198.5	39.1	682	10 AF401531	AF401531 Mus muscu
29	142	28.0	59554	9 AX695587	AX695587 Sequence
30	142	28.0	97075	9 AC010289	AC010289 Homo sapi
31	141.5	27.9	269	6 BD030595	BD030595 Sequence
32	139.5	27.5	527	10 AY046597	AY046597 Mus muscu
33	119	23.4	189981	2 AC137048	AC137048 Rattus no
34	119	23.4	209366	2 AC128918	AC128918 Rattus no
35	119	23.4	213593	2 AC131402	AC131402 Rattus no
36	119	23.4	245762	2 AC111422	AC111422 Rattus no
37	118	23.2	213593	2 AC131402	AC131402 Rattus no
38	118	23.2	273571	2 AC112851	AC112851 Rattus no
39	115	22.6	137334	10 AC121952	AC121952 Mus muscu
40	115	22.6	171595	2 AC121275	AC121275 Mus muscu
41	108	21.3	6283	6 AX252052	AX252052 Sequence
42	108	21.3	6283	6 AX344430	AX344430 Sequence
43	108	21.3	6283	6 AX346835	AX346835 Sequence
44	102	20.1	6283	6 AX252053	AX252053 Sequence
45	102	20.1	6283	6 AX344431	AX344431 Sequence

RESULT 1

ALIGNMENTS

BD085952
LOCUS BD085952 413 bp DNA linear PAT 27-AUG-2002
DEFINITION Elongation cDNA of secretory protein.
ACCESSION BD085952
VERSION BD085952.1 GI:22631562
KEYWORDS JP 2001523453-A/94.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Bougueleret, L., Duclert, A. and Edwards, J.B.D.M.
AUTHORS Bougueleret, L., Duclert, A. and Edwards, J.B.D.M.
TITLE Elongation cDNA of secretory protein
JOURNAL Patent: JP 2001523453-A 94 27-NOV-2001;
GENSET

COMMENT OS Homo sapiens (human)
PN JP 2001523453-A/94
PD 27-NOV-2001
PR 13-NOV-1998 JP 2000521191
PR 13-NOV-1997 US 60/066677,17-DEC-1997 US 60/069957 PR
09-FEB-1998 US 60/074121,13-APR-1998 US 60/081563 PR
10-AUG-1998 US 60/096116,04-SEP-1998 US 60/099273 PR
BOUGUELERET AYMERIC DUCLERT JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,PC
C12N1/21,
PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Von Heijne matrix
CC score 4.09999990463257
CC seq VFMLIVSVLALIP/ET
FH key Location/Qualifiers
FT sig_peptide 46..189
FT polyA_signal 377..382
FT polyA_site 402..413.
FT Location/Qualifiers
1..413
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 121 a 82 c 95 g 115 t

ORIGIN

Alignment Scores:
Pred. No.: 2.95e-56 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-801-115B-2 (1-99) x BD085952 (1-413)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 46 ATGGATTAACGTGACGCCGAAATATAACATCGCCCTTGTGCTTCACTGTAAGGAC 105
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 106 GTGAAGATGCGCGGCTGGATATTATCACTGATCACTGTAACAACAGATTTCATCTCATC 165
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 166 GTATCTGTGTGGACATGATACCGAAGAACCAACATTTGACAGTTGGTGGAGGGGTGTTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 226 GCACCTTGTGACGAGATGCTGCTTGGCGACGGGGCCCTTATTACCGAGACTTCTG 285
QY PheAsnProSerGlyProTyrGlnLysProValHisGluLysGluValLeu 99
DB 286 TTCAATCCACGCGGTCTTACCAAGAAAGAGCTGTGATGATAAAAAAGAGTTTGG 342

RESULT 2
AR306550
AR306550

LOCUS AR306550 515 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 29 from patent US 6548633.
ACCESSION AR306550
VERSION AR306550.1 GI:31696619
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 515)
TITLE Edwards, J.-B.D.M., Bougueleret, L. and Jobert, S.
JOURNAL Complementary DNA's encoding proteins with signal peptides
Patent: US 6548633-A 29 15-APR-2003;
FEATURES Location/Qualifiers
1..515
/organism="unknown"

BASE COUNT 143 a 106 c 135 g 130 t 1 others

ORIGIN

Alignment Scores:
Pred. No.: 3.88e-56 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-801-115B-2 (1-99) x AR306550 (1-515)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 144 ATGGATTAACGTGACGCCGAAATATAACATCGCCCTTGTGCTTCACTGTAAGGAC 203
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 204 GTGAAGATGCGCGGCTGGATATTATCACTGATCACTGTAACAACAGATTTCATCTCATC 263
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 264 GTATCTGTGTGGACATGATACCGAAGAACCAACATTTGACAGTTGGTGGAGGGGTGTTT 323
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 324 GCACCTTGTGACGAGATGCTGCTTGGCGACGGGGCCCTTATTACCGAGACTTCTG 383
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGluLysGluValLeu 99
DB 384 TTCAATCCACGCGGTCTTACCAAGAAAGAGCTGTGATGATAAAAAAGAGTTTGG 440

RESULT 3
AX061624 515 bp DNA linear PAT 24-JAN-2001
LOCUS AX061624
DEFINITION Sequence 29 from Patent WO0100806.
ACCESSION AX061624
VERSION AX061624.1 GI:12406709
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Homo sapiens
AUTHORS Homo sapiens
TITLE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
JOURNAL Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
GENSET (FR)

FEATURES Location/Qualifiers
1..515
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
144..443
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC24985.1"

/db_xref="GI:12406710"
/translation="MDNVQPKIHRPFCVKGHVYMLRDIINSLVTVFMLIVSVL
ALIPETTLTVGGVGFALVAVCCADGALIVRKLFPNPGPYOKRPVHEKKEVL"
144 . .287
/note="Von Heijne matrix score 4.10 seq VFMILIVSVLALIV/ET"
polya_signal 457 . .462
polya_site 500 . .515
BASE COUNT 143 a 106 c 135 g 130 t 1 others
ORIGIN

Alignment Scores:
Pred. No.: 3.88e-56 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-801-115B-2 (1-99) x AX061624 (1-515)

QY 1 MetAspAsnValGlnProLysIleLeuHisArgProPheCysPheSerValLysGlyHis 20
Db 144 ATGATTAAGTGTGACGCGGAAATTAACATCGCCCTTCTGCTTCACTGGAAGGCCAC 203

QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 204 GTCAAGATGCTGCGGCTGGATATTATCACTGTAACAACAGATTCAATGCTCATC 263

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 264 GTATCTGTGTGGACATGATACCAAGAACCAACATTTGACATGATGGAGGGGTGTTT 323

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleArgLysLeuLeu 80
Db 324 GCACCTGTGACAGCAGATGCTGTCTTCCGACGGGCGCTTATTTTCCGAAAGCTTCG 383

QY 81 PheAsnProSerGlyProTyrgLysProValHisGluLysGlyValLeu 99
Db 384 TTCATCCCGCGGCTCTTACCAAGAAAGCGCTGTGATGATGAAAAAGAGTTTGG 440

RESULT 4
AF096895 530 bp mRNA linear PRI 18-JUN-2001
LOCUS Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.
DEFINITION AF096895
ACCESSION AF096895.2 GI:9989691
VERSION
KEYWORDS FLI_CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 530)
Han,W., Lou,Y., Tang,J., Zhang,Y., Chen,Y., Li,Y., Gu,W., Huang,J.,
Gul,L., Tang,Y., Li,F., Song,Q., Di,C., Wang,L., Shi,Q., Sun,R.,
Xia,D., Rui,M., Tang,J., and Ma,D.
Molecular cloning and characterization of chemokine-like factor 1
(CKLF1), a novel human cytokine with unique structure and potential
chemoattractic activity
Biochem. J. 357 (Pt 1), 127-135 (2001)

JOURNAL MEDLINE
21308461
11415443
2 (bases 1 to 530)
Han,W.L., Li,Y., Zhang,Y.M., Di,C.H., Song,Q.S. and Ma,D.L.
Direct Submission
Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38
Xue Yuan Rd., Beijing 100083, China
3 (bases 1 to 530)
Han,W.L.
Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK
Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:6288733.

FEATURES
source Location/Qualifiers
1..530
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/note="exposed to phytohaemagglutinin (PHA)"
1..530
/gene="CKLF1"
/note="synonym: UCK-1"
148..447
/gene="CKLF1"
/note="increased expression in PHA stimulated cells;
expression inhibited by IL-10"
/codon_start=1
/product="chemokine-like factor 1"
/protein_id="AA06732.1"
/db_xref="GI:6288734"
/translation="MDNVQPKIHRPFCVKGHVYMLRDIINSLVTVFMLIVSVL
ALIPETTLTVGGVGFALVAVCCADGALIVRKLFPNPGPYOKRPVHEKKEVL"
BASE COUNT 156 a 108 c 137 g 129 t
ORIGIN

Alignment Scores:
Pred. No.: 4.02e-56 Length: 530
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AF096895 (1-530)

QY 1 MetAspAsnValGlnProLysIleLeuHisArgProPheCysPheSerValLysGlyHis 20
Db 148 ATGATTAAGTGTGACGCGGAAATTAACATCGCCCTTCTGCTTCACTGGAAGGCCAC 207

QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 208 GTCAAGATGCTGCGGCTGGATATTATCACTGTAACAACAGATTCAATGCTCATC 267

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 268 GTATCTGTGTGGACATGATACCAAGAACCAACATTTGACATGATGGAGGGGTGTTT 327

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleIleArgLysLeuLeu 80
Db 328 GCACCTGTGACAGCAGATGCTGTCTTCCGACGGGCGCTTATTTTCCGAAAGCTTCG 387

QY 81 PheAsnProSerGlyProTyrgLysProValHisGluLysGlyValLeu 99
Db 388 TTCATCCCGCGGCTCTTACCAAGAAAGCGCTGTGATGATGAAAAAGAGTTTGG 444

RESULT 5
AR275027 526 bp DNA linear PAT 10-APR-2003
LOCUS Sequence 164 from patent US 6506607.
DEFINITION AR275027
ACCESSION AR275027
VERSION AR275027.1 GI:29707577
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 526)
Shyjan,A.W.
Methods and compositions for the identification and assessment of
prostate cancer therapies and the diagnosis of prostate cancer
Patent: US 6506607-A 164 14-JAN-2003;
location/Qualifiers
1..526
/organism="unknown"
BASE COUNT 133 a 136 c 113 g 143 t 1 others
ORIGIN

source 1.500
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

BASE COUNT 135 a 102 c 125 g 129 t 9 others

ORIGIN

Alignment Scores:
Pred. No.: 1.05e-53 Length: 500
Score: 489.00 Matches: 98
Percent Similarity: 98.00% Conservative: 0
Best Local Similarity: 98.00% Mismatches: 1
Query Match: 96.26% Indels: 1
Gaps: 0

DB: 6

US-09-801-115b-2 (1-99) x BD085905 (1-500)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIyGlyHis 20
|||
Db 132 ATGGATTAACGTGACGCGGAAATATAACATCGCCCTTCGCTTCAGTGGAAAGGCCAC 191
|||
QY 21 ValMetLeuArgLeuAspIleLeuSerLeuValThrThrValPheMetLeu 40
|||
Db 192 GTGAGATGCTGGCTGGATTAATCACTCACTGTAACAACAGATTCATGCTCAT 251
|||
QY 40 eValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValAla 60
|||
Db 252 CGTATCTGTGTGACATGATGATCAAGAAACCAACAACATTGACAGTGTGGAGGGGTGT 311
|||
QY 60 eAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
|||
Db 312 TGCACTGTGACAGCAGTATGCTGTGGCGAGGGGCCCTTATTTACCGGAAGCTTCT 371
|||
QY 80 upheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
|||
Db 372 GTTCATATCCAGCGGCTCTTACCAAGAAAGCCTGTGATGAATAAAGAGTTTGG 429
|||

RESULT 7
AF057306 655 bp mRNA linear PRI 31-DEC-1999
LOCUS AF057306
DEFINITION Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.
ACCESSION AF057306
VERSION AF057306.1 GI:6648618
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 655)
REFERENCE Zhang, J.S., Nelson, M., Wang, L. and Smith D.I.
AUTHORS Direct Submission
JOURNAL Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic
and Foundation, Rochester, MN 55905, USA
FEATURES
source 1.655
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="AsPC-1"
/tissue_type="pancreas"
/note="adenocarcinoma"
1.655
/gene="C32"
132.590
/note="down regulated upon cell differentiation induced by
sodium butyrate"
/codon_start=1
/product="transmembrane proteolipid"
/protein_id="AAF2125.1"
/db_xref="GI:6648619"
/translation="MDNVQPKIKRPFQSVKGVKMLRLALVTSTMTFFLIQAQPP
YIVTGFETVILFFILLYVLRDLRLMKMLFPLDIINSIVTTFMLIVSVALIBE

TTTLTVGGVFALVTAVCCADGALTYRKLIENPSPGYOKKPYHEKEVYL"

BASE COUNT 171 a 137 c 153 g 194 t

ORIGIN

Alignment Scores:
Pred. No.: 2.66e-51 Length: 655
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
Gaps: 1

DB: 9

US-09-801-115b-2 (1-99) x AF057306 (1-655)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIyGlyHis 20
|||
Db 132 ATGGATTAACGTGACGCGGAAATATAACATCGCCCTTCGCTTCAGTGGAAAGGCCAC 191
|||
QY 21 ValMetLeuArg----- 25
|||
Db 192 GTGAGATGCTGGCTGGATTAATCACTCACTGTAACAACAGATTCATGCTTTTATCATGCA 251
|||
QY 25 ----- 25
|||
Db 252 GCCCTGACCAATATATTGTTATCACTGATTTGAAGTCAACCGTTATCTATTTTTCATA 311
|||
QY 26 -----LeuAsp 27
|||
Db 312 CTTTATATGATCTACAGACTTGATCGATTATGAAGTATTATTTGGCTTGCCTTGAT 371
|||
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
|||
Db 372 ATTATCACTCACTGATGTAACAACAGATTCATGCTCATCTGATCTGTGGACATGATA 431
|||
QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
|||
Db 432 CCAAGAACCAACAACATTGACAGTGTGGAGGGGTGTTCACCTGTGACAGCAGTATGC 491
|||
QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87
|||
Db 492 TGCTTGTCCACAGCGGCGCTTATTTACCGGAAGCTTGTTCATATCCACGCGTCTTAC 551
|||
QY 88 GlnLysLysProValHisGluLysGluValLeu 99
|||
Db 552 CAGAAAGCCCTGTGATGAATAAAGAGTTTGG 587
|||

RESULT 8
AR306591 669 bp DNA linear PAT 12-JUN-2003
LOCUS AR306591
DEFINITION Sequence 70 from patent US 6548633.
ACCESSION AR306591
VERSION AR306591.1 GI:31696660
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 669)
AUTHORS Edwards, J. B. D. M., Bougueleret, L. and Jobert, S.
JOURNAL Complementary DNA's encoding proteins with signal peptides
TITL Patent: US 6548633-A 70 15-APR-2003;
JOURNAL Location/Qualifiers
FEATURES
source 1.669
/organism="unknown"
BASE COUNT 178 a 139 c 158 g 194 t
ORIGIN

Alignment Scores:
Pred. No.: 2.73e-51 Length: 669
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
Gaps: 1

US-09-801-115B-2 (1-99) x AR306591 (1-669)

QY 1 MetAspAsnValGlnProIySileYshHsArgProPheCysPheSerVallySGlyHis 20
Db 140 ATGGATACCTGACGCGGAAATAAACATCGCCCTTCTGCTTCAAGTGAAGGCGCAC 199

QY 21 ValIysMetLeuArg----- 25
Db 200 GTGAAGATGCTGGCGGCTGGCAGCTACTGTGACATCTATGACCTTTTATCATGCGACAA 259

QY 25 ----- 25
Db 260 GCCCGTGAACCATATATTGTTATCATGATTGAAGTACCGTTATCTTATTTTCATA 319

QY 26 -----LeuAsp 27
Db 320 CTTTATATGACTCAGACTTGATCGATTAAATGAAGGTATTATTTGGCCTTCTTGAT 379

QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaIle 47
Db 380 ATTATCACTCACTGCTGTTACACAGATATTCTCATCTCATCTGCTTGGCAGTATA 439

QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 440 CCAGAAACCAACAACATTGACAGTTGGTGGAGGGGTGTTGCACCTTGACAGCAGTATGC 499

QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgIysLeuLeuPheAsnProSerGlyProTyr 87
Db 500 TGTCTTCCGACGGGGCCCTTATTATTCGGAAGCTTCTGTTCATCCAGCGGTCTTAC 559

QY 88 GlnIysLysProValHisGluLysLysGluValIleu 99
Db 560 CAGAAAAAGCCTGTGCATGAATAAAAAAGAGTTTGG 595

RESULT 9
LOCUS AX061665 669 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 70 from Patent WO0100806.
ACCESSION AX061665
VERSION AX061665.1 GI:12406789
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1
AUTHORS dumas mine Edwards, J.B., Bougueteloret, I. and Jobert, S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 70 04-JAN-2001;
GENSET (PR)

FEATURES
Location/Qualifiers
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140..598
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/codon start=1
/protein id="CAC25025.1"
/db xref="GI:12406790"
/translation="MDNVQPKIKRPFCEYKGVKMLRLATVTSMTFFIIQAAPP
YIVTGPETVYILFFILLXVRLRLMKMLFPLDITINSIVTVPMILYVALIIE
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CDS
sig_peptide
140..442
/note="Von Heijne matrix score 4.10 seq VFMLIVSLALIP/ET"
polyA_signal
630..635
polyA_site
655..669
BASE COUNT 178 a 139 c 158 g 194 t
ORIGIN

Alignment Scores:
Pred. No.: 2.73e-51 Length: 669

Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 53
Query Match: 92.81% Indels: 1
DB: 6 Gaps: 1

US-09-801-115B-2 (1-99) x AX061665 (1-669)

QY 1 MetAspAsnValGlnProIySileYshHsArgProPheCysPheSerVallySGlyHis 20
Db 140 ATGGATACCTGACGCGGAAATAAACATCGCCCTTCTGCTTCAAGTGAAGGCGCAC 199

QY 21 ValIysMetLeuArg----- 25
Db 200 GTGAAGATGCTGGCGGCTGGCAGCTACTGTGACATCTATGACCTTTTATCATGCGACAA 259

QY 25 ----- 25
Db 260 GCCCGTGAACCATATATTGTTATCATGATTGAAGTACCGTTATCTTATTTTCATA 319

QY 26 -----LeuAsp 27
Db 320 CTTTATATGACTCAGACTTGATCGATTAAATGAAGGTATTATTTGGCCTTCTTGAT 379

QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaIle 47
Db 380 ATTATCACTCACTGCTGTTACACAGATATTCTCATCTCATCTGCTTGGCAGTATA 439

QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
Db 440 CCAGAAACCAACAACATTGACAGTTGGTGGAGGGGTGTTGCACCTTGACAGCAGTATGC 499

QY 68 CysLeuAlaAspGlyAlaLeuIleTyrArgIysLeuLeuPheAsnProSerGlyProTyr 87
Db 500 TGTCTTCCGACGGGGCCCTTATTATTCGGAAGCTTCTGTTCATCCAGCGGTCTTAC 559

QY 88 GlnIysLysProValHisGluLysLysGluValIleu 99
Db 560 CAGAAAAAGCCTGTGCATGAATAAAAAAGAGTTTGG 595

RESULT 10
LOCUS BC004380 688 bp mRNA linear PRI 12-JUN-2001
DEFINITION Homo sapiens, clone MGC:10658 IMAGE:3639550, mRNA, complete cds.
ACCESSION BC004380
VERSION BC004380.1 GI:13325133
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 688)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK
COMMENT NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ULNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Buterfield,
Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guo,
Leticia Hsiao, Martin Krzywincki, Reta Kutsche, Oliver Lee, Sui
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Nees, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smaluis, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marita.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/INL at: <http://image.lnl.gov>
Series: IRAL Plate: 13 Row: f Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9989692.
Location/Qualifiers

FEATURES
source

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/db_xref="taxon:9606"
/clone="MGC:10658 IMAGE:3619550"
/issue_type="Pancreas, adenocarcinoma"
/clone_id="NIH MGC_39"
/lab_host="DH10B-R"
/note="Vector: pOT87"
137..595
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/db_xref="GI:13325134"
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BASE COUNT
ORIGIN

201 a 138 c 154 g 195 t

Alignment Scores:

Pred. No.: 2.82e-51 Length: 688
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x BC004380 (1-688)

QY 1 MetAspAsnValGlnProLysIleLeuGlnArgProPheCysPheSerValIysGlyHis 20
DB 137 ATGGATACGTGACGCCGAAATTAACATCGCCCTTCCTTCAGTGGAAAGGCCAC 196
QY 21 ValIysMetLeuArg----- 25
DB 197 GTGAAGATGCTGGCGGCTGGCACTAGTGCATCTATGACCTTTTATCATGCACAA 256
QY 25 ----- 25
DB 257 GCCCGTAACATATATTGTTATCATGATTGAAGTCAACCGTTATCTTATTTTCATA 316
QY 26 -----LeuAsp 27
DB 317 CTTTATATGACTACAGACTGATCGATTAAATGAAGGTTATTTGGCCTTGCTTGAT 376
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47
DB 377 ATTATCACTCACTGCTGTAACAAGCTATTCATGCTCATCTGATCTGTTGGCACTGATA 436
QY 48 ProGluThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
DB 437 CCGAAACCAACAACATTTGACAGTTGGTGGAGGGGTGTTTGCACCTTGACAGCAGTATGC 496
QY 68 CysLeuAlaAspGlyAlaLeuIleTyThrArgLysLeuLeuPheAsnProSerGlyProTyr 87
DB 497 TGTCTTCCGACGGGGCCCTTATTTTACCGAAGCTTCCTGTTCAATCCAGGCGCTTAC 556
QY 88 GlnLysLysProValHisGluLysGluValLeu 99
DB 557 CAGAAAAGCCTGTGCATGAAAAAAGAGATTTC 592
RESULT 11
AF135380

LOCUS AF135380 689 bp mRNA linear PRI 07-SEP-2000
DEFINITION Homo sapiens chemokine-like factor 2 (CKLF2) mRNA, complete cds,
alternatively spliced.
ACCESSION AF135380
VERSION AF135380.2 GI:9989692
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 689)
Han, W.L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.
Direct Submission
Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
2 (bases 1 to 689)
Han, W.L.
Direct Submission
Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:6630853.
Location/Qualifiers

REFERENCE

AUTHORS
TITLE
JOURNAL

REFERENCE

AUTHORS
TITLE
JOURNAL

REMARK

COMMENT
FEATURES

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1..689
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
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148..606
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/note="UCK-2, alternatively spliced"
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/db_xref="GI:6630854"
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TTTLVGGGVFALVTAVCCADGALLYRKLLFNPSGPYQKKPVHEKKEVL"

CDS

gene
CDS

BASE COUNT
ORIGIN

195 a 140 c 161 g 193 t

Alignment Scores:

Pred. No.: 2.83e-51 Length: 689
Score: 471.50 Matches: 99
Percent Similarity: 65.13% Conservative: 0
Best Local Similarity: 65.13% Mismatches: 0
Query Match: 92.81% Indels: 53
DB: 9 Gaps: 1

US-09-801-115B-2 (1-99) x AF135380 (1-689)

QY 1 MetAspAsnValGlnProLysIleLeuGlnArgProPheCysPheSerValIysGlyHis 20
DB 148 ATGGATACGTGACGCCGAAATTAACATCGCCCTTCCTTCAGTGGAAAGGCCAC 207
QY 21 ValIysMetLeuArg----- 25
DB 208 GTGAAGATGCTGGCGGCTGGCACTAGTGCATCTATGACCTTTTATCATGCACAA 267
QY 25 ----- 25
DB 268 GCCCGTAACATATATTGTTATCATGATTGAAGTCAACCGTTATCTTATTTTCATA 327
QY 26 -----LeuAsp 27
DB 328 CTTTATATGACTACAGACTGATCGATTAAATGAAGGTTATTTGGCCTTGCTTGAT 387
QY 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47

Db	388	ATTATCACTACGTCGTAAACAAGATATTCATGCTCATCGTATCTGTGTGCACTGATA	447
Qy	48	ProGluThrThrThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys	67
Db	448	CCAGAAACCAACAACATTGACAGTTGGTGGAGGGGTTTGACATTGTGACGACGATAGC	507
Qy	68	CysLeuAlaaspGlyAlaLeuIleIleTyrArgLysLeuLeuPheAsnProSerGlyProTyr	87
Db	508	TGTCTTCCGACGGGGCCCTTATTATCCGGAAGCTTCTGTTCAATCCAGCGTCTTAC	567
Qy	88	GlnYsLysProValHisGlnLysLysGluValIleu	99
Db	568	CAGAAAAAGCCGTGTCATGAAAAAAAAGAAATTGG	603
RESULT 12			
LOCUS	BD023892	415 bp	DNA
DEFINITION	Sequence tag and encoded human protein.	linear	PAT 27-AUG-2002
ACCESSION	BD023892		
VERSION	BD023892.1	GI:22565115	
KEYWORDS	JP 2001269182-A/138.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	1 (bases 1 to 415)		
TITLE	Edwards,J.B.D.M., Duclair,E. and Jordan,J.Y.		
JOURNAL	Sequence tag and encoded human protein		
COMMENT	Patent: JP 2001269182-A 138 02-OCT-2001;		
	GENSET		
	OS Homo sapiens (human)		
	PN JP 2001269182-A/138		
	PD 02-OCT-2001		
	PF 24-FEB-2000 JP 2000118773		
	PR 26-FEB-1999 US 60/122487		
	PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES JORDAN		
	PI C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC C12N5/10,		
	PC C12P21/02, C12P21/08, C12Q1/68, //G06F17/30, C12N15/00, C12N5/00, PC G06F15/40		
	CC score 4.1		
	CC seq VFMILVSVLALIP/ET		
	PH key	Location/Qualifiers	
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	FT sig_peptide	146..289.	
	FT Location/Qualifiers		
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ORIGIN			91 t
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Pred. No.:	3,41e-50	Length:	415
Score:	461.00	Matches:	90
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	90.75%	Indels:	0
DB:	6	Gaps:	0
US-09-801-115B-2 (1-99) x BD023892 (1-415)			
Qy	1	MetAspaenValGlnProLysIleLeuHisArgProPheCysPheSerValLysGlyHis	20
Db	146	ATGCAATACGTCACCCGAAAAATAAAAATCGCCCCCTTCTGCTTCAAGTGAAGGCGAC	205
Qy	21	ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle	40
Db	206	GTTGAAGATCGTCGGCTGGATATTATCAACTACACGTGTAACAACAGTATTATGCTATC	265
Qy	41	ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe	60

Db	266	GTATCTGTGTGGACATGATACCAAGAAACCAACAACATTGACAGTTGGTGGAGGGGTGTTT	325
Oy	61	AlAlenValIhrrAlaValCysCysGleAlaAlaSGClYAlAlenUleTyrrArglySleUleU	80
Db	326	GCACCTTGTCAGACAGATGCTCTCTTCGCGACGGGGCCCTTATTACCGAAGCTTCTG	385
Oy	81	PhaenProSeSrgIyProTyrgInUlyLys	90
Db	386	TTCAATCCAGCGGTCTTACCAAGAAAAG	415
RESULT 13			
LOCUS	G30204/c	485 bp	DNA linear STS 05-OCT-1996
DEFINITION	human STS SHGC-36487, sequence tagged site.		
ACCESSION	G30204		
VERSION	G30204.1	GI:1593755	
KEYWORDS	STS; STS sequence; primer; sequence tagged site.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 485)		
JOURNAL	Myers,R.M.		
COMMENT	Unpublished (1996)		
	Contact: Richard M. Myers		
	Stanford Human Genome Center (SHGC)		
	Stanford University School of Medicine		
	Department of Genetics, M-344, Stanford, CA 94305, USA		
	Tel: 4157259687		
	Fax: 4157259689		
	Email: myers@shgc.stanford.edu		
	Primer A: ACTCTTTTTCATGACACAG		
	Primer B: GCCCTATTTCACGAGACT		
	STS size: 77		
	PCR Profile:		
	Initial incubation: 94 degrees C for 90 seconds		
	Denaturation: 94 degrees C for 15 seconds		
	Annealing: 62 degrees C for 23 seconds		
	Polymerization: 72 degrees C for 30 seconds		
	PCR Cycles: 30		
	Thermal Cycler: Perkin Elmer 9600		
	Protocol:		
	Template: 25 ng		
	Primer: each 1 uM		
	dNTPs: each 200 uM		
	Tag Polymerase: 0.05 units/uI		
	Total Vol: 10 uI		
	Buffer:		
	MgCl2: 2.5 mM		
	KCl: 50 mM		
	Tris-HCl: 20 mM		
	pH: 8.3		
FEATURES			
source	1..485		
	Location/Qualifiers		
	1..485		
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	69..91		
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	complement(126..145)		
	146 a	99 c	99 g
	131 t	10	others
BASE COUNT	146 a	99 c	99 g
ORIGIN			
Alignment Scores:			

Pred. No.: 7.32e-38 Length: 485
Score: 366.00 Matches: 73
Percent Similarity: 98.65% Conservative: 0
Best Local Similarity: 98.65% Mismatches: 1
Query Match: 72.05% Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x G30204 (1-485)

QY 26 LeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValIleuAla 45
Db 286 CTGATATTTCACCTACCTGCTACACAGTATTCATGCTCATCGTANCTGTTGGCA 227
QY 46 LeuIleProGluThrThrThrIleuThrValGlyGlyValPheAlaIleuValThrAla 65
Db 226 CTGATACCAAGAACACACACATTGACAGTGTGTGAGAGGGGTGTTGCACTTGACAGCA 167
QY 66 ValCysCysLeuAlaAspGlyAlaIleuIleTyThrArgLysLeuLeuPheAsnProSerGly 85
Db 166 GTATGCTGTCTTCCGACGGGGCCCTTATTACCGGAAGCTTCTGTCATCCACGCGGT 107
QY 86 ProTyGlnLysLysProValHisGluLysGluValLeu 99
Db 106 CTTTACCAGAAAAGCTGTGCAATGAAAAAGAAAGTTTG 65

RESULT 14

AF145216 593 bp mRNA linear PRI 07-SEP-2000
LOCUS Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF145216
VERSION AF145216.2 GI:9989694
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 593)
Han, W.L., Gu, W.F., Li, Y., Zhang, Y.M., Di, C.H., Song, Q.S. and
Ma, D.L.

TITLE Direct Submission
JOURNAL Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue
AUTHORS Yuan Road, Beijing 100083, China
REFERENCE 2 (bases 1 to 593)
Han, W.L.

JOURNAL Direct Submission
TITLE Submitted (07-SEP-2000) Immunology, Peking University Health
AUTHORS Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK Sequence update by submitter
COMMENT On Sep 7, 2000 this sequence version replaced gi:6625671.
FEATURES
location/Qualifiers

source

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/cell_line="U937"
/note="from PHA stimulated cells"
1..593
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/note="synonym: UCK"
148..510
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/note="UCK-4; alternatively spliced"
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NPSGPYKRVVHEKEVTL"

gene

CDS

BASE COUNT 166 a 120 c 140 g 167 t
ORIGIN

Alignment Scores:
Pred. No.: 2.45e-34 Length: 593
Score: 339.50 Matches: 73
Percent Similarity: 61.90% Conservative: 5
Best Local Similarity: 57.94% Mismatches: 15
Query Match: 66.83% Indels: 33
DB: 9 Gaps: 2

US-09-801-115B-2 (1-99) x AF145216 (1-593)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 148 ATGATACAGCTGACGAGCGAAATATAACATCGCCCTTCTGCTTCAGTGTGAAGGCCAC 207
QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 208 GTGAAGATCTGTGGGTGGACACTA-----ACTGTGACATCATATGACC 249
QY 41 ValSerValLeuAlaIleuIleProGluThrThrThrLeuThrValGlyGly----- 58
Db 250 TTTTATTATCATGCACAGCCCTGAAACCATATATTGTTATCATCTGATTGAAGTCACC 309
QY 58 ----- 58
Db 310 GTTATCTTATTCTTTCACACTTTTATATGATCATCATGATGATTAATGAAGTGTTA 369
QY 59 -----ValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAla 73
Db 370 TTTTGACCTTGTGCTTGTGTTGACCTTGACAGCAGTATGCTGTTCGCCAGGGGGCC 429
QY 74 LeuIleTyThrArgLysLeuLeuPheAsnProSerGlyProTyGlnLysLysProValHis 93
Db 430 CTTATTACCGGAAGCTCTGTTCAATCCACAGCGGTCTTACAGAAAAAGCCTGTGCAT 489
QY 94 GluLysGluValLeu 99
Db 490 GAAAAAAGAAAGTTTG 507

RESULT 15

AF135381 434 bp mRNA linear PRI 07-SEP-2000
LOCUS Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,
DEFINITION alternatively spliced.
ACCESSION AF135381
VERSION AF135381.2 GI:9989693
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 434)
Han, W.L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.

TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
AUTHORS Yuan Road, Beijing 100083, China
REFERENCE 2 (bases 1 to 434)
Han, W.L.

JOURNAL Direct Submission
TITLE Submitted (07-SEP-2000) Immunology, Peking University Health
AUTHORS Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK Sequence update by submitter
COMMENT On Sep 7, 2000 this sequence version replaced gi:6630855.
FEATURES
location/Qualifiers

source

1..434
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
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/gene="CKLF3"
/note="UCK"
148..351

gene

CDS

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/gene="CKLF3"  
/note="uCK-3: alternatively spliced"  
/codon_start=1  
/product="chemokine-like factor 3"  
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ORIGIN
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Alignment Scores:  
Pred. No.:      2.08e-33      Length:      434  
Score:      331.00      Matches:      67  
Percent Similarity:      67.68%      Conservative:      0  
Best Local Similarity:      67.68%      Mismatches:      0  
Query Match:      65.16%      Indels:      32  
DB:      9      Gaps:      1
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US-09-801-115b-2 (1-99) x AF135381 (1-434)

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QY      1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20  
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Db      148 ATGGATTAACGTGCAGCCGAAATAAATCAATGCCCCCTTCTTCAGTGTAAGGCCAC 207  
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QY      21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40  
      |||  
Db      208 GTGAAGATGCTGCGGCTG----- 225  
      |||  
QY      41 ValSerValLeuAlaLeuIleProGlnThrThrThrLeuThrValGlyGlyValPhe 60  
      |||  
Db      226 -----GTGTTT 231  
      |||  
QY      61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80  
      |||  
Db      232 GCACTTGGACAGCAGTATGCTGCTTGGCCGACGGGGCCCTTATTACCGAAGCTTCTG 291  
      |||  
QY      81 PheAsnProSerGlyProTyrGlnLysLysProValHisGlnLysGluValLeu 99  
      |||  
Db      292 TTCATCCACGGGCTTACCAAGAAAGAGCTGTGATGAGAAAGAAAGATTGTTG 348
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Search completed: January 31, 2004, 04:50:56
Job time : 1820 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2004, 04:16:13 ; Search time 273 Seconds
(without alignments)
1321.652 Million cell updates/sec

Title: US-09-801-115B-2
Perfect score: 508
Sequence: 1 MDVQPKIKRPFCSYKVG.....LFPNSGPKYKKPVHEKKEVL 99

Scoring table:
BLOSUM62 Xgapop 10.0 , Xgapext 0.5
Xgapop 10.0 , Ygapext 0.5
Xgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2434939 seqs, 1822278265 residues
Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-TRANS=human40.cdi -DIST=45 -DCCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:*

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16:	/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
17:	/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
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1	508	100.0	413	13	US-10-319-763-147	Sequence 147, App
2	508	100.0	422	11	US-09-918-993-6534	Sequence 6534, App
3	508	100.0	439	11	US-09-822-846-397	Sequence 397, App
4	508	100.0	504	11	US-09-809-391-98	Sequence 98, App
5	508	100.0	504	13	US-09-882-171-98	Sequence 98, App
6	508	100.0	506	11	US-09-809-391-252	Sequence 252, App
7	508	100.0	506	13	US-09-882-171-252	Sequence 252, App
8	508	100.0	534	9	US-09-801-115-1	Sequence 1, App
9	508	100.0	558	15	US-10-106-698-1927	Sequence 1927, App
10	508	100.0	655	12	US-10-291-172-13	Sequence 13, App
11	508	100.0	817	13	US-10-119-428-14	Sequence 14, App
12	502	98.8	512	11	US-09-918-995-19489	Sequence 19489, App
13	489	96.3	500	13	US-10-319-763-53	Sequence 53, App
14	472	92.9	400	12	US-10-242-535A-7940	Sequence 7940, App
15	471.5	92.8	459	9	US-09-801-115-3	Sequence 3, App
16	471.5	92.8	663	10	US-09-978-295A-189	Sequence 189, App
17	471.5	92.8	663	10	US-09-978-697-189	Sequence 189, App
18	471.5	92.8	663	10	US-09-978-192A-189	Sequence 189, App
19	471.5	92.8	663	10	US-09-999-832A-189	Sequence 189, App
20	471.5	92.8	663	11	US-09-978-189-189	Sequence 189, App
21	471.5	92.8	663	11	US-09-978-608A-189	Sequence 189, App
22	471.5	92.8	663	11	US-09-978-585A-189	Sequence 189, App
23	471.5	92.8	663	11	US-09-978-191A-189	Sequence 189, App
24	471.5	92.8	663	11	US-09-978-403A-189	Sequence 189, App
25	471.5	92.8	663	11	US-09-978-564A-189	Sequence 189, App
26	471.5	92.8	663	11	US-09-999-833A-189	Sequence 189, App
27	471.5	92.8	663	11	US-09-981-915A-189	Sequence 189, App
28	471.5	92.8	663	11	US-09-978-824-189	Sequence 189, App
29	471.5	92.8	663	11	US-09-978-585A-189	Sequence 189, App
30	471.5	92.8	663	11	US-09-978-423A-189	Sequence 189, App
31	471.5	92.8	663	11	US-09-978-193A-189	Sequence 189, App
32	471.5	92.8	663	11	US-09-999-830A-189	Sequence 189, App
33	471.5	92.8	663	11	US-09-978-187B-189	Sequence 189, App
34	471.5	92.8	663	11	US-09-978-187B-189	Sequence 189, App
35	471.5	92.8	663	11	US-09-978-642A-189	Sequence 189, App
36	471.5	92.8	663	12	US-10-013-912A-189	Sequence 189, App
37	471.5	92.8	663	12	US-10-013-920A-189	Sequence 189, App
38	471.5	92.8	663	12	US-10-145-093A-189	Sequence 189, App
39	471.5	92.8	663	13	US-09-978-375A-189	Sequence 189, App
40	471.5	92.8	663	13	US-09-978-188A-189	Sequence 189, App
41	471.5	92.8	663	13	US-09-978-298A-189	Sequence 189, App
42	471.5	92.8	663	13	US-10-143-031A-189	Sequence 189, App
43	471.5	92.8	663	13	US-10-002-967A-189	Sequence 189, App
44	471.5	92.8	663	13	US-10-017-083A-189	Sequence 189, App
45	471.5	92.8	663	13	US-10-143-030A-189	Sequence 189, App

ALIGNMENTS

RESULT 1
US-10-319-763-147
Sequence 147, Application US/10319763
Publication No. US20030144490A1
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Ducleert, Aymeric
TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 147
LENGTH: 413
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 46..189
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.0999990463257
OTHER INFORMATION: seq VFMLIVSLALIP/ET
FEATURE:
NAME/KEY: polyA_signal
LOCATION: 377..382
FEATURE:
NAME/KEY: polyA_site
LOCATION: 402..413
US-10-319-763-147

Alignment Scores:
Pred. No.: 4,97e-64 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-801-115B-2 (1-99) x US-10-319-763-147 (1-413)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20
DB 46 ATGATTAACGTGCAGCGCAAAATAAACATCGCCCTCTCTCAGTGTAAAGGCAC 105
QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 106 GTGAGATGCTGCGCGCTGGAATATTATCACTCACTGTAACAACAAGATTATCTCATC 165
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 166 GTACTGTGTGGACATCATACCAAAACCAACATTGACATGGTGGAGGGGTGTTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 226 GCACCTGTGACAGAGATGCTGCTTGCACGCGGGCCCTTATTATCCGGAACTTCTG 285
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGluLysGluValLeu 99
DB 286 TTCAATCCACGCGGTCTTACCAAGAAAGCCTGTGATGAAAAAGAAAGTTTGG 342

RESULT 2

US-09-918-995-6534
Sequence 6534, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6534
LENGTH: 422
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-6534
Alignment Scores:
Pred. No.: 5.13e-64 Length: 422

Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-918-995-6534 (1-422)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20
DB 31 ATGATTAACGTGCAGCGCAAAATAAACATCGCCCTCTCTCAGTGTAAAGGCAC 90
QY 21 ValIleMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 91 GTGAGATGCTGCGCGCTGGAATATTATCACTCACTGTAACAACAAGATTATCTCATC 150
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 151 GTACTGTGTGGACATCATACCAAAACCAACATTGACATGGTGGAGGGGTGTTT 210
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 211 GCACCTGTGACAGAGATGCTGCTTGCACGCGGGCCCTTATTATCCGGAACTTCTG 270
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGluLysGluValLeu 99
DB 271 TTCAATCCACGCGGTCTTACCAAGAAAGCCTGTGATGAAAAAGAAAGTTTGG 327

RESULT 3

US-09-822-846-397
Sequence 397, Application US/09822846
Publication No. US20030027139A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fecthel, Kim
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
APPLICANT: Gulukota, Kamalakkar
APPLICANT: Graham, James R.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REFERENCE: GIN 6400
CURRENT APPLICATION NUMBER: US/09/822,846
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,605
PRIOR FILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 397
LENGTH: 439
TYPE: DNA
ORGANISM: Homo sapiens
US-09-822-846-397
Alignment Scores:
Pred. No.: 5.44e-64 Length: 439
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-822-846-397 (1-439)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIlySGIYHis 20
Db 81 ATGGATTAACGTGACGCGGAAATTAACATCGCCCTTCTGCTTCACTGCGAAAGCCAC 140

QY 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 141 GTGAAGATGCTGGCGGTGATATTAATCACTGATCACTGGTAACAACAGATTATCATGCTCATC 200

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 201 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTTGGTGAGGGGTGTTT 260

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyValaLeuIleIlyrArgIlyLeu 80
Db 261 GCACCTGTGACAGATGATGCTGTGCTTGGCGAGGGGCGCTTATTTACCGAAAGCTTCTG 320

QY 81 PheAsnProSerGlyProIlyrGlnIlyLysProValHisGluIlyLysGluValLeu 99
Db 321 TTCATCCAGCGGTCTCTTACGAAAGCCTGTGTGATATAAAAAAGAGTTTGG 377

RESULT 4

US-09-809-391-98
; Sequence 98, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-98

Alignment Scores:

Pred. No.:	6,68e-64	Length:	504
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-809-391-98 (1-504)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIlySGIYHis 20
Db 131 ATGGATTAACGTGACGCGGAAATTAACATCGCCCTTCTGCTTCACTGCGAAAGCCAC 150

QY 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 191 GTGAAGATGCTGGCGGTGATATTAATCACTGATCACTGGTAACAACAGATTATCATGCTCATC 250

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 251 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTTGGTGAGGGGTGTTT 310

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyValaLeuIleIlyrArgIlyLeu 80
Db 311 GCACCTGTGACAGATGATGCTGTGCTTGGCGAGGGGCGCTTATTTACCGAAAGCTTCTG 370

QY 81 PheAsnProSerGlyProIlyrGlnIlyLysProValHisGluIlyLysGluValLeu 99
Db 371 TTCATCCAGCGGTCTCTTACGAAAGCCTGTGTGATATAAAAAAGAGTTTGG 427

RESULT 5

US-09-882-171-98
; Sequence 98, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 98
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-882-171-98

Alignment Scores:

Pred. No.:	6,68e-64	Length:	504
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	11	Gaps:	0

US-09-801-115B-2 (1-99) x US-09-809-391-98 (1-504)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIlySGIYHis 20
Db 131 ATGGATTAACGTGACGCGGAAATTAACATCGCCCTTCTGCTTCACTGCGAAAGCCAC 150

QY 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 191 GTGAAGATGCTGGCGGTGATATTAATCACTGATCACTGGTAACAACAGATTATCATGCTCATC 250

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 251 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGACAGTTGGTGAGGGGTGTTT 310

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyValaLeuIleIlyrArgIlyLeu 80
Db 311 GCACCTGTGACAGATGATGCTGTGCTTGGCGAGGGGCGCTTATTTACCGAAAGCTTCTG 370

QY 81 PheAsnProSerGlyProIlyrGlnIlyLysProValHisGluIlyLysGluValLeu 99
Db 371 TTCATCCAGCGGTCTCTTACGAAAGCCTGTGTGATATAAAAAAGAGTTTGG 427

RESULT 5

;; PRIOR APPLICATION NUMBER: 60/043,580
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,568
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,314
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,569
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,311
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,671
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,674
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;; PRIOR APPLICATION NUMBER: 60/043,669
;; PRIOR FILING DATE: 1997-04-11
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;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,672
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,315
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/048,974
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/056,886
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,877
;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,662
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,872
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,882
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,637
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,903
;; PRIOR FILING DATE: 1997-08-22
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;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,845
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,892
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/057,761

;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/047,595
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,599
;; PRIOR FILING DATE: 1997-05-23
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;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,585
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,586
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,590
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,594
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,589
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,593
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/047,614
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/043,578
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/043,576
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/047,501
;; PRIOR FILING DATE: 1997-05-23
;; PRIOR APPLICATION NUMBER: 60/043,670
;; PRIOR FILING DATE: 1997-04-11
;; PRIOR APPLICATION NUMBER: 60/056,632
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,664
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,876
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,881
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,909
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,875
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,862
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,887
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,908
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/048,964
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/057,650
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/056,884
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/057,669
;; PRIOR FILING DATE: 1997-09-05

Alignment Scores:

;; Align. No.: 6,68e-64 Length: 504
;; Score: 508.00 Matches: 99
;; Percent Similarity: 100.00% Conservative: 0
;; Best Local Similarity: 100.00% Mismatches: 0
;; Query Match: 100.00% Indels: 0
;; DB: 13 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-882-171-98 (1-504)

Qy 1 MetAspAsnValGlnProLysIleTySH1sArGProPhaCysPheSerValIysG1yH1s 20
Db 131 ATGATTAACCTGACGCGAAATAAACAATCGCCCTTGTGCTCACTGTAAGCCAC 190
Qy 21 ValIysMetIeuArgIeuAepIleIleAsnSerIeuValThrValIysMetIeuIle 40
Db 191 GTGAAGATGCTGCGCTGATATTATCACTCACTGTAACAACAGTATTCAATGCTCATC 250

QY 41 ValSerValIleuAlaIleuIleProGluThrThrIleuThrValGlyGlyValPhe 60
| | | | |
Db 251 GTATCTGTGTGGACGATGATACCAAGAACCAATGACGTTGTGGAGGGGTCTT 310
QY 61 AlaIleuValThrAlaValCysCysIleuAlaAspGlyAlaIleuIleYrArgIysIleu 80
| | | | |
Db 311 GCACCTGTGACAGAGATATGCTGTCTTCCGACGGGGCCCTTATTATCCGGAAGCTTCTG 370
QY 81 PheAsnProSerGlyProTyrGlnIlyIysProValHisGlyIysIysGluValIleu 99
| | | | |
Db 371 TTCAATCCAGCGGTCTTACAGAAAAGCCTGTGATGATAAAGAGATTG 427

RESULT 6
US-09-809-391-252
; Sequence 252, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 252
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-809-391-252

Alignment Scores:
Pred. No.: 6 72e-64 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-801-115b-2 (1-99) x US-09-809-391-252 (1-506)

QY 1 MetAspAsnValGlnProIysIleIysHisArgProPheCysPheSerValIysGlyHis 20
| | | | |
Db 117 ATGATTAACGTGCGCCGGAATAAATGATGCCCCCTTCTGCTTCAAGTGAAGGCCAC 176
QY 21 ValIysMetIeuArgIeuAspIleIleAsnSerIeuValThrThrValPheMetIleu 40
| | | | |
Db 177 GTGAAGATGCTGCGCGCTGATATATCACTCACTGGTAACACAGATATTCATCTCATC 236
QY 41 ValSerValIleuAlaIleuIleProGluThrThrIleuThrValGlyGlyValPhe 60
| | | | |
Db 237 GTATCTGTGTGGACGATGATACCAAGAACCAATGACGTTGTGGAGGGGTCTT 296
QY 61 AlaIleuValThrAlaValCysCysIleuAlaAspGlyAlaIleuIleYrArgIysIleu 80
| | | | |
Db 297 GCACCTGTGACAGAGATATGCTGTCTTCCGACGGGGCCCTTATTATCCGGAAGCTTCTG 356
QY 81 PheAsnProSerGlyProTyrGlnIlyIysProValHisGlyIysIysGluValIleu 99
| | | | |
Db 357 TTCAATCCAGCGGTCTTACAGAAAAGCCTGTGATGATAAAGAGATTG 413

RESULT 7
US-09-882-171-252
; Sequence 252, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391

PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 09/149,476
PRIOR FILING DATE: 1998-09-08
PRIOR APPLICATION NUMBER: PCT/US98/04493
PRIOR FILING DATE: 1998-03-06
PRIOR APPLICATION NUMBER: 60/040,162
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,333
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/038,621
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,626
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,334
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,336
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/040,163
PRIOR FILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: 60/047,600
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,615
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,597
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,502
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,633
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,583
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/047,617
PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,580
PRIOR FILING DATE: 1997-04-11
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,569
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,311
PRIOR FILING DATE: 1997-04-11

PRIOR APPLICATION NUMBER: 60/043,671
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,674
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,669
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,312
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/043,313
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PRIOR FILING DATE: 1997-05-23
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PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/047,501
PRIOR FILING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: 60/043,670
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: 60/056,632
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,664
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PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,881
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,909
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,875
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,862
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,887
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/056,908
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/048,964
PRIOR FILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/057,650
PRIOR FILING DATE: 1997-09-05
PRIOR APPLICATION NUMBER: 60/056,884
PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: 60/057,669
PRIOR FILING DATE: 1997-09-05

Alignment Scores:

Fred. No.: 6,72e-64 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Dbs: 13 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-882-171-252 (1-506)

Qy 1 MetaspasnaValaGlnProLySileLySAsrProPheCysPheSerValLySgLYHis 20
Db 117 ATGATTAACGTGCAGCGGAAATTAACATCGCCCTTCGTGCTGATGGAAGGCCAC 176
Qy 21 ValiysMetLeuLyrgLeuaspIlelleAsnSerLeuValThrValPheMetLeuIle 40
Db 177 GTGAAGATGCTGGCGGCTGGATATTATCACTGATTAACAACAGATATTCATGCTCATC 236
Qy 41 ValSerValLeuValaleuIleProGluThrThrThrLeuThrValGlyGlyValAlphe 60
Db 237 GTATCTGTGTGGACGATGACCAAGAACCAACATGACAGTTGGTGGAGGGGTGTTT 236
Qy 61 AlaleuValThrAlaValCysCysLeuAlaaspGlyAlaleuIleTyArgLySLeuLeu 80
Db 297 GCACCTTGACAGCAGATGCTGTCTTCCGACGGGCCCTTATTATCCGGAAGCTTCTG 356
Qy 81 PheAsnProSerGlyProTyrgInLySProValHisGluLySgIuValLeu 99

Db 357 TTCATCCAGCGGCTCTTACAGAAAAAGCTGTGATGAAAAAAGAGTTTGG 413

RESULT 8

US-09-801-115-1

Sequence 1, Application US/09801115

Patent No. US2002001828A1

GENERAL INFORMATION:

APPLICANT: Ma, D.

APPLICANT: Han, W.

APPLICANT: Zhang, Y.

APPLICANT: Song, Q.

APPLICANT: Di, C.

APPLICANT: Huang, J.

APPLICANT: Tang, J.

APPLICANT: Chen, G.

TITLE OF INVENTION: CHEMOKINE LIKE FACTOR (CKLF) WITH CHEMOTACTIC AND HEMATOPOIETIC

TITLE OF INVENTION: STIMULATING ACTIVITIES

FILE REFERENCE: 10776-003-999

CURRENT APPLICATION NUMBER: US/09/801,115

PRIOR FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: PCT/CN06/00026

PRIOR FILING DATE: 2000-02-15

PRIOR APPLICATION NUMBER: 99107284.7

PRIOR FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 8

SEQ ID NO 1

LENGTH: 534

TYPE: DNA

ORGANISM: Homo sapiens

US-09-801-115-1

Alignment Scores:

Pred. No.: 7,29e-64 Length: 534

Score: 508.00 Matches: 99

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-801-115-1 (1-534)

Qy 1 MetaspasnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20

Db 152 ATGATTAACGTGACGCGGAAATTAACATGCCCCCTTCTGCTTCAAGTGAAAGGCCAC 211

Qy 21 ValIysMetLeuArgLeuAspIleIleasnSerLeuValThrThrValPheMetLeuIle 40

Db 212 GTGAAGATGCTGCGCGCTGATATTATCAACTCAGCTGTAAACAAGATATTCATGCTCATC 271

Qy 41 ValSerValIleuAlaIleuIleProGlnThrThrLeuThrValGlyGlyValPhe 60

Db 272 GTATCTGTGTGGACATGATACCAAGAAACCAACATTGAAGTTGGTGGAGGGGTGTTT 331

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyArgLysLeu 80

Db 332 GCACTTGTGAAGACGATGCTGCTTCCGACGGGGCCCTATTATTACCGAAGCTTCTG 391

Qy 81 PheasnProSerGlyProTyArgLysLeuProValHisGlyLysGlyValIleu 99

Db 392 TTCATCCAGCGGCTCTTACAGAAAAAGCTGTGATGAAAAAAGAGTTTGG 448

RESULT 9

US-10-106-698-1927

Sequence 1927, Application US/10106698

Publication No. US20030109690A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide

FILE REFERENCE: PA005P1

CURRENT APPLICATION NUMBER: US/10/106,698

PRIOR FILING DATE: 2002-03-27

PRIOR APPLICATION NUMBER: PCT/US00/26524

PRIOR FILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US 60/157,137

PRIOR FILING DATE: 1999-09-29

PRIOR APPLICATION NUMBER: US 60/163,280

PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564

SOFTWARE: Patentm Ver. 3.0

SEQ ID NO 1927

LENGTH: 558

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (514)..(514)

OTHER INFORMATION: n equals a,t,g, or c

US-10-106-698-1927

Alignment Scores:

Pred. No.: 7,78e-64 Length: 558

Score: 508.00 Matches: 99

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 15 Gaps: 0

US-09-801-115B-2 (1-99) x US-10-106-698-1927 (1-558)

Qy 1 MetaspasnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20

Db 147 ATGATTAACGTGACGCGGAAATTAACATGCCCCCTTCTGCTTCAAGTGAAAGGCCAC 206

Qy 21 ValIysMetLeuArgLeuAspIleIleasnSerLeuValThrThrValPheMetLeuIle 40

Db 207 GTGAAGATGCTGCGCGCTGATATTATCACTCATGTTAAACAAGATATTCATCTCATC 266

Qy 41 ValSerValIleuAlaIleuIleProGlnThrThrLeuThrValGlyGlyValPhe 60

Db 267 GTATCTGTGTGGACATGATACCAAGAAACCAACATTGAAGTTGGTGGAGGGGTGTTT 326

Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyArgLysLeu 80

Db 327 GCACTTGTGAAGACGATGATGCTTCCGACGGGGCCCTATTATTACCGAAGCTTCTG 386

Qy 81 PheasnProSerGlyProTyArgLysLeuProValHisGlyLysGlyValIleu 99

Db 387 TTCATCCAGCGGCTCTTACAGAAAAAGCTGTGATGAAAAAAGAGTTTGG 443

RESULT 10

US-10-291-172-13

Sequence 13, Application US/10291172

Publication No. US20030228584A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc

TITLE OF INVENTION: No. US20030228584A1el Nucleic Acids and Polypeptides

FILE REFERENCE: 21272-045

CURRENT APPLICATION NUMBER: US/10/291,172

PRIOR FILING DATE: 2000-11-08

PRIOR APPLICATION NUMBER: 09/693,267

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 09/665,363

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 09/616,847

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: 09/596,193

PRIOR FILING DATE: 2000-06-17

PRIOR APPLICATION NUMBER: 09/574,454

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: 09/519,705

PRIOR FILING DATE: 2000-03-07

NUMBER OF SEQ ID NOS: 752

SEQ ID NO 13

LENGTH: 655

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (134)..(430)
US-10-291-172-13

Alignment Scores:

Pred. No.:	9,89e-64	Length:	655
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	12	Indels:	0
DB:	12	Gaps:	0

US-09-801-115b-2 (1-99) x US-10-291-172-13 (1-655)

Qy 1 MetAspAsnValGlnProIysIleIySHISARGProPhCySePheSerValIySGIYHIS 20
Db 134 ATGGATACGTGACGCCGAAATAAACATCGCCCTTGCTTCAGTGGAAAGGCCAC 193
Qy 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 194 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACAAGATTTCATCTCATC 253
Qy 41 ValSerValIleuAlaIleuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 254 GATCTGTGTGGCAGTGAATACCAAGAAACCAACATTGACAGTTGGAGGGGTTT 313
Qy 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaIleuIleTyrrArgIySLeu 80
Db 314 GCACCTGTGACAGACGATATGCTGTTCGCCGACGGGCCCTTATTATTCGGAAGCTTCTG 373
Qy 81 PheAsnProSerGlyProTyrrGlnIySlySProValHisGluIySlySGIuValIleu 99
Db 374 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAAAAAGAGTTTGG 430

RESULT 11

US-10-119-428-14

Sequence 14, Application US/10119428
Publication No. US20030165881A1

GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Xu, Chongjun
APPLICANT: Wehman, Tom
APPLICANT: Ren, Feiyan
APPLICANT: Ma, Yungqing
APPLICANT: Zhou, Ping
APPLICANT: Zhao, Yonghong
APPLICANT: Dmanac, Radoje T.
TITLE OF INVENTION: No. US20030165881A1el Nucleic Acids and
FILE REFERENCE: 789CIP2
CURRENT APPLICATION NUMBER: US/10/119,428
CURRENT FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 09/596,193
PRIOR FILING DATE: 2000-06-17
PRIOR APPLICATION NUMBER: 09/574,454
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: 09/519,705
PRIOR FILING DATE: 2000-03-07
NUMBER OF SEQ ID NOS: 55
SOFTWARE: pc_fla_genes Version 1.0
SEQ ID NO 14
LENGTH: 817
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (236)..(535)
US-10-119-428-14

Alignment Scores:

Pred. No.:	1.38e-63	Length:	817
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13	Indels:	0
DB:	13	Gaps:	0

US-09-801-115b-2 (1-99) x US-10-119-428-14 (1-817)

Qy 1 MetAspAsnValGlnProIysIleIySHISARGProPhCySePheSerValIySGIYHIS 20
Db 236 ATGGATACGTGACGCCGAAATAAACATCGCCCTTGCTTCAGTGGAAAGGCCAC 295
Qy 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 296 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACAAGATTTCATCTCATC 355
Qy 41 ValSerValIleuAlaIleuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 356 GATCTGTGTGGCAGTGAATACCAAGAAACCAACATTGACAGTTGGAGGGGTTT 415
Qy 61 AlaLeuValThrAlaValAlaCysCysLeuAlaAspGlyAlaIleuIleTyrrArgIySLeu 80
Db 416 GCACCTGTGACAGACGATATGCTGTTCGCCGACGGGCCCTTATTATTCGGAAGCTTCTG 475
Qy 81 PheAsnProSerGlyProTyrrGlnIySlySProValHisGluIySlySGIuValIleu 99
Db 476 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAAAAAGAGTTTGG 532

RESULT 12

US-09-918-995-19489

Sequence 19489, Application US/09918995
Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19489
LENGTH: 512
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(512)
OTHER INFORMATION: n = A, T, C or G
US-09-918-995-19489

Alignment Scores:

Pred. No.:	5.08e-63	Length:	512
Score:	502.00	Matches:	98
Percent Similarity:	98.99%	Conservative:	0
Best Local Similarity:	98.99%	Mismatches:	1
Query Match:	11	Indels:	0
DB:	11	Gaps:	0

US-09-801-115b-2 (1-99) x US-09-918-995-19489 (1-512)

Qy 1 MetAspAsnValGlnProIysIleIySHISARGProPhCySePheSerValIySGIYHIS 20
Db 142 ATGGATACGTGACGCCGAAATAAACATCGCCCTTGCTTCAGTGGAAAGGCCAC 201
Qy 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 202 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACAAGATTTCATCTCATC 261

Qy	4	ValSerValIleuValIleuLeuIleProGluThrThrThrIleThrValGlyValIlePhe	60
Db	262	GTATCTGTGTGGCACTGATACCAAGAAACCAACATTCACAGTTGGTGGAGGGGTGTT	322
Qy	61	AlaIleuValThrAlaValAlaCysCysLeuAlaAspGlyAlaIleuLeuIleTyrArgLysLeuIleu	80
Db	322	GCACCTGTGTGACACAGATATCTGTCTTGGCCGAGGGGGCCCTTATTATCCGGAAGCTTGTG	381
Qy	81	PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValIleu	99
Db	382	TTCAATCCGACGGGTCTTACCAAGAAAAAGCCTGTGCATGAAAAAAGAGTTTG	438
RESULT 13			
US-10-319-763-53			
Sequence 53, Application US/10319763			
Publication No. US20030144490A1			
GENERAL INFORMATION:			
APPLICANT: Dumas Milne Edwards, Jean-Baptiste			
APPLICANT: Duclert, Aymeric			
APPLICANT: Bougueleret, Lydie			
TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS			
FILE REFERENCE: G-031.US04.DIV			
CURRENT APPLICATION NUMBER: US/10/319,763			
PRIOR FILING DATE: 2002-12-10			
PRIOR APPLICATION NUMBER: 60/066,677			
PRIOR FILING DATE: 1997-11-13			
PRIOR APPLICATION NUMBER: 60/069,957			
PRIOR FILING DATE: 1997-12-17			
PRIOR APPLICATION NUMBER: 60/074,121			
PRIOR FILING DATE: 1998-02-09			
PRIOR APPLICATION NUMBER: 60/081,563			
PRIOR FILING DATE: 1998-04-13			
PRIOR APPLICATION NUMBER: 60/096,116			
PRIOR FILING DATE: 1998-08-10			
PRIOR APPLICATION NUMBER: 60/099,273			
PRIOR FILING DATE: 1998-09-04			
NUMBER OF SEQ ID NOS: 229			
SOFTWARE: Patent.pm			
SEQ ID NO 53			
LENGTH: 500			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURE:			
NAME/KEY: sig_peptide			
LOCATION: 199..288			
OTHER INFORMATION: Von Heijne matrix			
OTHER INFORMATION: score 5.59999990463257			
OTHER INFORMATION: seq IVSVALIPEPTT/LT			
FEATURE:			
NAME/KEY: polyA_signal			
LOCATION: 464..469			
FEATURE:			
NAME/KEY: polyA_site			
LOCATION: 489..500			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: 197..412			
OTHER INFORMATION: homology			
OTHER INFORMATION: id :AA429945			
OTHER INFORMATION: est			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: 61..195			
OTHER INFORMATION: homology			
OTHER INFORMATION: id :AA429945			
OTHER INFORMATION: est			
FEATURE:			
NAME/KEY: misc_feature			
LOCATION: 425..488			
OTHER INFORMATION: homology			
OTHER INFORMATION: id :AA429945			
OTHER INFORMATION: est			

FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 197_412	
OTHER INFORMATION: homology	
OTHER INFORMATION: id :AA4550422	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 61_195	
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OTHER INFORMATION: id :AA4550422	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
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OTHER INFORMATION: id :AA4550422	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 207_412	
OTHER INFORMATION: homology	
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OTHER INFORMATION: est	
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NAME/KEY: misc_feature	
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OTHER INFORMATION: homology	
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OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 425_488	
OTHER INFORMATION: homology	
OTHER INFORMATION: id :W93646	
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FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 197_412	
OTHER INFORMATION: homology	
OTHER INFORMATION: id :AA516433	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 90_195	
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OTHER INFORMATION: id :AA516433	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 425_488	
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OTHER INFORMATION: id :AA516433	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 52_195	
OTHER INFORMATION: homology	
OTHER INFORMATION: id :W38899	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 197_324	
OTHER INFORMATION: homology	
OTHER INFORMATION: id :W38899	
OTHER INFORMATION: est	
FEATURE:	
NAME/KEY: misc_feature	
LOCATION: 443_477	
OTHER INFORMATION: homology	
OTHER INFORMATION: id :W38899	
OTHER INFORMATION: est	

NAME/KEY: misc_feature
LOCATION: 197..338
OTHER INFORMATION: homology
OTHER INFORMATION: id:M52820
FEATURE:
NAME/KEY: misc_feature
LOCATION: 71..195
OTHER INFORMATION: homology
OTHER INFORMATION: id:M52820
OTHER INFORMATION: est
FEATURE:
NAME/KEY: misc_feature
LOCATION: 339..401
OTHER INFORMATION: homology
OTHER INFORMATION: id:M52820
OTHER INFORMATION: est
FEATURE:
NAME/KEY: misc_feature
LOCATION: 425..469
OTHER INFORMATION: homology
OTHER INFORMATION: id:M52820
OTHER INFORMATION: est
FEATURE:
NAME/KEY: misc_feature
LOCATION: 40..195
OTHER INFORMATION: homology
OTHER INFORMATION: id:M52820
OTHER INFORMATION: est
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9..10,12
OTHER INFORMATION: n=a, g, c or t
US-10-319-763-53

Alignment Scores:
Pred. No.: 3,77e-61 Length: 500
Score: 489.00 Matches: 98
Percent Similarity: 98.00% Conservative: 0
Best Local Similarity: 98.00% Mismatches: 1
Query Match: 96.26% Indels: 1
DB: 13 Gaps: 0

US-09-801-115b-2 (1-99) x US-10-319-763-53 (1-500)

QY 1 MetAspAsnValGlnProIysIleIySHiARgProPhCySpheSerValIySgIyHIs 20
DB 132 ATGATTAACGTGCGAGCGGAAATTAACATCGCCCTTCTGCTTCACTGTAAGGCGCAC 191
QY 21 ValIyMetLeuArgLeuAspIleIeAsnSerLeuValThrValPheMetLeuI 40
DB 192 GTGATGATGCTGGCGCTGATATTAACAACCTGTAACAACAGTATTCATGCTCAT 251
QY 40 eValSerValIleuAlaLeuIleProGluThrThrLeuThrValIySgIyValPh 60
DB 252 CGATATCTGTGGCACTGATACCAAGAACCAACATTTGCTGAGAGGGGTGT 311
QY 60 eAlaLeuValThrAlaValIyCySgLeuAlaAspGlyAlaLeuIleIyTrArgIySLeu 80
DB 312 TGCCTTGTGACAGCAGTATGCTCTCTTCCGAGGGGCGCTTATTACCGGAGCTTCT 371
QY 80 upheAsnProSerGlyProIyGlnIySgIySgProValIySgIyValIySgIyValIy 99
DB 372 GTTCAATCCAGCGGCTCTTACCAAGAAAGAGCTGTGATGAAAGAAAGAGTTTG 429

RESULT 14
US-10-242-535A-7940
Sequence 7940, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Lew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 7940
LENGTH: 400
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (176)..(176)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-7940

Alignment Scores:
Pred. No.: 7.91e-59 Length: 400
Score: 472.00 Matches: 94
Percent Similarity: 97.92% Conservative: 0
Best Local Similarity: 97.92% Mismatches: 1
Query Match: 92.91% Indels: 1
DB: 12 Gaps: 0

US-09-801-115b-2 (1-99) x US-10-242-535A-7940 (1-400)

QY 1 MetAspAsnValGlnProIysIleIySHiARgProPhCySpheSerValIySgIyHIs 20
DB 115 ATGATTAACGTGCGAGCGGAAATTAACATCGCCCTTCTGCTTCACTGTAAGGCGCAC 174
QY 21 ValIyMetLeuArgLeuAspIleIeAsnSerLeuValThrValPheMetLeuI 40
DB 175 GNGAAGATGTGCGCTGATATTAACAACCTGTAACAACAGTATTCATGCTCATC 234
QY 41 ValSerValIleuAlaLeuIleProGluThrThrLeuThrValIySgIyValPhe 60
DB 235 GTATCTGTGTGGCACTGATACCAAGAACCAACATTTGCACTGTGAGGGGTGT 294
QY 61 AlaLeuValThrAlaValIyCySgLeuAlaAspGlyAlaLeuIleIyTrArgIySLeu 80
DB 295 GCACCTTGTGACGAGTATGCTCTTCCGAGGGGCGCTTATTACCGGAGCTTCT 354
QY 80 upheAsnProSerGlyProIyGlnIySgIySgProValIySgIyValIySgIyValIy 95
DB 355 GTTCAATCCAGCGGCTCTTACCAAGAAAGAGCTGTGATGAAAGAAAGAGTTTG 400

RESULT 15
US-09-801-115-3
Sequence 3, Application US/09801115
Patent No. US2002001828A1
GENERAL INFORMATION:
APPLICANT: Ma, D.
APPLICANT: Han, W.
APPLICANT: Zhang, Y.
APPLICANT: Song, Q.
APPLICANT: Di, C.
APPLICANT: Huang, J.
APPLICANT: Tang, J.
TITLE OF INVENTION: CHEMOKINE LIKE FACTOR (CLF) WITH CHEMOTACTIC AND HEMATOPOIETIC
STIMULATING ACTIVITIES
FILE REFERENCE: 10776-003-999
CURRENT APPLICATION NUMBER: US/09/801,115
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/CN00/00026
PRIOR FILING DATE: 2000-02-15

? PRIOR APPLICATION NUMBER: 99107284.7
 ? PRIOR FILING DATE: 1999-05-14
 ? NUMBER OF SEQ ID NOS: 8
 ? SEQ ID NO: 3
 ? LENGTH: 459
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US-09-801-115-3

Alignment Scores:	
Pred. No.:	1,15e-58
Score:	471.50
Percent Similarity:	65.13%
Best local Similarity:	65.13%
Query Match:	92.81%
DB:	9
	Gaps: 1
	length: 459
	Matches: 99
	Conservative: 0
	Mismatches: 0
	Indels: 53
	Gaps: 1

US-09-801-115B-2 (1-99) X US-09-801-115-3 (1-459)

QY	1	MeAspAsnValGlnProIysIleuYshSaGpProPheCysPheSerValIysGluHis	20
Db	1	ATGATGATACGTCGACGCCGAAATAAACAATGCCCCCTTCCTCAGGTGAAGGCCAC	60
QY	21	ValIysMeIeuArg	25
Db	61	GTCAGATGCTGGCGCTGGCACAACCTGACATCATGACCTTTTATCATGCACAA	120
QY	25	-----	25
Db	121	GCCCCGTGAACCATATATTGTTATCACTGSAATTGAAAGTACCGTTACTTATTTTCATA	180
QY	26	-----LeuAsp	27
Db	181	CTTTATATGTACTCAGACCTGATCGATTAATGAAGTGGTATATTTGGCCTTTGCTTGAT	240
QY	28	IleIleAsnSerIeuValThrThrValPheMetIeuIleValSerValIeuIleLeuIle	47
Db	241	ATTATCAACTCAGCTGGTAACAACAGTATTCACAGCTCATCGATCTGGTGGCACTGATA	300
QY	48	ProGluThrThrThrIeuThrValGlyGlyGlyValPheAlaIeuValThrAlaValCys	67
Db	301	CCAGAAACCACAACATTGACAGTGGTGSAGGGGCTTTGCACCTTGACACGACGTATGC	360
QY	68	CysIeuAlaAspGlyAlaIeuIleTyrArgIysIeuIeuPheAsnProSerGlyProTyr	87
Db	361	TGTCCTGGCCGACCGGGCCCTTATTTTACCGGAAGCTTCGTTCATACCCAGCGGTCCTTAC	420
QY	88	GlnIysIeuProValHisGluIysIysGluValIleu	99
Db	421	CAGAAAAGCCTGTGCATGAAAAAAGAAAGTTTGG	456

Search completed: January 31, 2004, 05:31:41
Job time : 275 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame.p2n model

Run on: January 31, 2004, 04:11:13 ; Search time 74 Seconds
(without alignments)
590.499 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508
Sequence: 1 MDNVQPKIKRPFCSYVGH.....LFNDSGPYQKKPVHEKKEVL 99

Scoring table: BIOSUM62

Xgapop 10.0 ,	Xgapext 0.5
Ygapop 10.0 ,	Ygapext 0.5
Delop 6.0 ,	Fgapext 7.0
Delop 6.0 ,	Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO_spool_p/US09801115/runat_30012004_113849_7051/app_query.fasta.1.263
-DB=issued_patents_NA -QFMT=fastap -SUFFIX=p2n.rnt -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=BIOSUM62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR MAX=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09801115 @CGN 1.1 103 @runat 30012004_113849_7051 -NCPU=6 -ICPU=3
-NO_MMAP -LARGOQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=130 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCFUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	508	100.0	413	4	US-09-663-600A-147
2	508	100.0	504	4	US-09-149-476-98
3	508	100.0	506	4	US-09-149-476-252
4	508	100.0	515	4	US-09-599-360B-29
5	491	96.7	526	4	US-09-220-132-164
6	489	96.3	500	4	US-09-663-600A-53
7	471.5	92.8	669	4	US-09-599-360B-70
8	357	70.3	392	3	US-09-385-982-95
9	83	16.3	37948	3	US-09-251-646-11
10	73	14.4	1083	3	US-09-116-498-11
11	73	14.4	1083	4	US-09-170-496D-179
12	71	14.0	1083	3	US-09-116-498-7

13	71	14.0	1083	4	US-09-170-496D-27	Sequence 27, Appl
14	71	14.0	1232	4	US-09-016-434-1079	Sequence 1079, Ap
15	66.5	13.1	720	1	US-08-061-092A-2	Sequence 2, Appl1
16	66	13.0	4403765	3	US-09-103-840A-2	Sequence 1, Appl1
17	66	13.0	4411529	3	US-09-103-840A-1	Sequence 12, Appl
18	65.5	12.9	43676	3	US-09-356-952-12	Sequence 1, Appl1
19	65	12.8	3872	4	US-09-165-396-1	Sequence 9, Appl1
20	64.5	12.7	1333	1	US-08-684-862-9	Sequence 1, Appl1
21	64.5	12.7	2211	3	US-09-462-844-1	Sequence 14, Appl
22	64.5	12.7	7721	3	US-08-772-770A-14	Sequence 1, Appl1
23	64.5	12.7	1664976	4	US-08-916-421B-1	Sequence 1, Appl1
24	64	12.6	1278	4	US-09-107-532A-2920	Sequence 2920, Ap
25	64	12.6	17710	4	US-08-976-359-70	Sequence 70, Appl
26	64	12.6	25165	4	US-09-453-702B-39	Sequence 39, Appl
27	63.5	12.5	654	3	US-08-998-416-176	Sequence 176, App
28	63.5	12.5	1785	3	US-09-377-155-8	Sequence 8, Appl1
29	63.5	12.5	1785	4	US-09-669-974-8	Sequence 8, Appl1
30	63.5	12.5	2153	4	US-09-367-206-6	Sequence 6, Appl1
31	63	12.4	1818	4	US-09-252-991A-7778	Sequence 7778, Ap
32	63	12.4	1854	1	US-08-249-420-1	Sequence 1, Appl1
33	63	12.4	1854	2	US-08-737-663-1	Sequence 1, Appl1
34	63	12.4	2241	4	US-09-252-991A-7562	Sequence 7562, Ap
35	63	12.4	4403765	3	US-09-103-840A-2	Sequence 2, Appl1
36	63	12.3	4411529	3	US-09-103-840A-1	Sequence 1, Appl1
37	62.5	12.3	615	4	US-09-134-001C-376	Sequence 376, App
38	62.5	12.3	1105	4	US-09-221-017B-108	Sequence 108, App
39	62.5	12.3	9711	4	US-08-961-527-167	Sequence 167, App
40	62	12.2	745	4	US-08-221-017B-319	Sequence 319, App
41	62	12.2	819	4	US-08-309-182B-2	Sequence 2, Appl1
42	62	12.2	6943	4	US-09-453-702B-213	Sequence 213, App
43	61.5	12.1	1327	6	US320941-1	Patent No. 5320941
44	61.5	12.1	1435	2	US-08-878-989-14	Sequence 14, Appl
45	61.5	12.1	1435	3	US-09-272-796-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-663-600A-147
; Sequence 147, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; TITLE OR INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 147
; LENGTH: 413
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 46..189
; OTHER INFORMATION: Von Heijne matrix

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; OTHER INFORMATION: score 4.09999990463257
; OTHER INFORMATION: seq VFMLIVSLALIP/ET
; NAME/KEY: polyA signal
; LOCATION: 377..382
; NAME/KEY: polyA site
; LOCATION: 402..413
; US-09-663-600A-147

Alignment Scores:
Pred. No.: 2,33e-66 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-663-600A-147 (1-413)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
Db 46 ATGGATACGCTGACGCGGAAATATAACATCGCCCTTCTGCTTCACTGGTGAAGGCCAC 105
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 106 GTGAAGAGTGGCGGCTGGATATTATCACTGATGTAACACAGATTCAATGCTCATC 165
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 166 GTACTCTGTTGGACGATGATACGAAACCAACATTGACAGTGTGAGGGGCTTTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
Db 226 GCACTGTGACAGCAGATGCTGCTTGGCCGCGGGCCCTTATTATCCGGAAGCTTCTG 285
QY 81 PheAsnProSerGlyProTyrGlnLysLeuProValHisGluLysGluValLeu 99
Db 286 TTCAATCCAGCGGTCTCTTACGAAAGAGCTTGTGATGAAAAAGAGTTTGG 342

RESULT 2
US-09-149-476-98
; Sequence 98. Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149, 476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
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; EARLIER APPLICATION NUMBER: 60/040,336
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; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,584
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,596
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/043,314
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; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
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EARLIER APPLICATION NUMBER: 60/056,662
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EARLIER APPLICATION NUMBER: 60/056,637
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EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,888
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,879
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EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,599
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EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,585
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EARLIER APPLICATION NUMBER: 60/047,586
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,590
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,594
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,589
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,593
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,578
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909

EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,875
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Alignment Scores:
Pred. No.: 3,14e-66 Length: 504
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-149-476-98 (1-504)

QY 1 MetAspAsnValGlnProIysIleIysHISarxProPhcCysPheSerValIysGlyHIS 20
DB 131 ATGATTAACCTGACGCCGAAATATAAATACATCGCCCTTCTGCTTCACTGTAAGGCCAC 190

QY 21 ValIysMetLeuArgIleuAspIleIleAsnSerLeuValThrThyValPheMetLeuIle 40
DB 191 GTGAGATGTGTGGGTGGATATTATCACTCACTGTAACACACAGATTATCATGCTCATC 250

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThleuThyValGlyValPhe 60
DB 251 GTATCTGTGTGGCTGATACACGAAACCAACATTAAGCTGTGTGAGGGGTGTTT 310

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleThrArgIysLeu 80
DB 311 GCACCTGTGACACAGATGCTGTCTTGCAGGAGGCCCTTATTTACCGAAGCTTTCTG 370

QY 81 PheAsnProSerGlyProTyrGlnIysLysProValHISGluIysIysGluValLeu 99
DB 371 TTCATCCACGGCGTCTTACGAAAGAGCCGTGTCATGAAAAAGAGATTG 427

RESULT 3
US-09-149-476-252
Sequence 252, Application US/09149476
Patent No. 6420526
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 186 Human Secreted proteins
FILE REFERENCE: P2002PI
CURRENT APPLICATION NUMBER: US/09/149,476
CURRENT FILING DATE: 1998-09-08
EARLIER APPLICATION NUMBER: PCT/US98/04493
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,626
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334

[illegible]

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EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/047,501
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER FILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,664
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,876
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,881
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
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EARLIER APPLICATION NUMBER: 60/056,875
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EARLIER APPLICATION NUMBER: 60/056,887
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EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/057,650
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
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EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02
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Alignment Scores:
Pred. No.: 3,15e-66 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-801-115B-2 (1-99) x US-09-149-476-252 (1-506)

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QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 117 ATGGATTAACGTGACGCGAATAATTAACATCGCCCTTCTGCTTCAAGTGAAGGCCAC 176
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 177 GTGAAGATGCTGCGCGCTGATATTATCACTCACTGTAAACAAGATTATCATCTCATC 236
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 237 GTACTCTGTGTGGACATGATCCAGAAACCAACATTGACAGTGTGGAGGGGTGTT 296
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 297 GCACCTGTGACAGATAGTCTGTCTGCGACGGGGCCCTTATTATCCGGAAGCTTCTG 356
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluValLysGluValLeu 99
DB 357 TTCAATCCACGCGGTCTTACCAAGAAAAGCTGTGATGAAAAAAGAGTTTGG 413
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RESULT 4
US-09-599-3608-29
; Sequence 29 Application US/09599360B
; Patent No. 6548633
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Bouguetieret, L.
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APPLICANT: Ubert, S.
; TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
; FILE REFERENCE: GENSET.050CP3
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 29
LENGTH: 515
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 144..440
NAME/KEY: sig_peptide
LOCATION: 144..287
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.10
NAME/KEY: polyA_signal
LOCATION: 457..462
NAME/KEY: polyA_site
LOCATION: 500..515
NAME/KEY: misc_feature
LOCATION: 60
OTHER INFORMATION: n=a, g, c or t
US-09-599-3608-29
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Alignment Scores:
Pred. No.: 3,24e-66 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
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US-09-801-115B-2 (1-99) x US-09-599-3608-29 (1-515)

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QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 144 ATGGATTAACGTGACGCGAATAATTAACATCGCCCTTCTGCTTCAAGTGAAGGCCAC 203
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 204 GTGAAGATGCTGCGCGCTGATATTATCACTCACTGTAAACAAGATTATCATCTCATC 263
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 264 GTACTCTGTGTGGACATGATCCAGAAACCAACATTGACAGTGTGGAGGGGTGTT 323
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 324 GCACCTGTGACAGATAGTCTGTCTGCGACGGGGCCCTTATTATCCGGAAGCTTCTG 383
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluValLysGluValLeu 99
DB 384 TTCAATCCACGCGGTCTTACCAAGAAAAGCTGTGATGAAAAAAGAGTTTGG 440
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RESULT 5
US-09-220-132-164/c
; Sequence 164 Application US/09220132
; Patent No. 6506607
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND ASSESSMENT
; OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
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;; CURRENT APPLICATION NUMBER: US/09/220,132
;; CURRENT FILING DATE: 1998-12-23
;; PRIOR APPLICATION NUMBER: US 60/079,303
;; PRIOR FILING DATE: 1998-03-25
;; PRIOR APPLICATION NUMBER: US 60/068,821
;; PRIOR FILING DATE: 1997-12-24
;; NUMBER OF SEQ ID NOS: 191
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 164
;; LENGTH: 526
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: misc_feature
;; LOCATION: (1)..(526)
;; OTHER INFORMATION: n = A,T,C or G
US-09-220-132-164

Alignment Scores:
Pred. No.: 1,12e-63 Length: 526
Score: 491.00 Matches: 98
Percent Similarity: 98.99% Conservative: 0
Best Local Similarity: 98.99% Mismatches: 0
Query Match: 96.65% Indels: 1
DB: 4 Gaps: 0

US-09-801-115B-2 (1-99) x US-09-220-132-164 (1-526)

QY 1 MetaspantValGlnProlyllylelyHisArg-ProthecyspheserVallylGlyHl 20
Db 370 ATGGATTAACGTGCACGCCCAATAAATACATCGGCCCTTCCTGCTCATGTGAAGGCCA 311
QY 20 GVallyswetleuArgleuAspIleleAsnSerleuValThrThrValPheMetleuIl 40
Db 310 CGTGAAGATGCTGCAGCTGATTAATCACTCACTGTAACAACAGATTCACTCAT 251
QY 40 eValserValleuAlaLeuileprogluThrThrThrleuThrValglyglyValAlph 60
Db 250 CGTATCTGTGTGGCAGTATACGAAACCAACATGACAGTGTGAGGGGTGT 191
QY 60 eAlaleuValThrAlaValCyGcSleuAlaAspGlyAlaLeuileTyraGlySleuLe 80
Db 190 TGCACCTGTGACAGCAGATATCTGTCTTGCACGCGGCCCTTATTATACCGAAGCTTCT 131
QY 80 uPhaAsnProserGlyProTyrglnlyValProValHsglnlyslsglyVal 98
Db 130 GTTCATCCAGCGGCTCTTACGAAAGCGCTGTGATGAAAAAGAGATT 76

RESULT 6
US-09-663-600A-53
;; Sequence 53, Application US/09663600A
;; Patent No. 6573068
;; GENERAL INFORMATION:
;; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
;; APPLICANT: Duclert, Aymeric
;; APPLICANT: Bousquelert, Lydie
;; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
;; FILE REFERENCE: 31.US3.CIP
;; CURRENT APPLICATION NUMBER: US/09/663,600A
;; CURRENT FILING DATE: 2000-09-15
;; PRIOR APPLICATION NUMBER: 09/191,997
;; PRIOR FILING DATE: 1998-11-13
;; PRIOR APPLICATION NUMBER: 60/066,677
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: 60/069,957
;; PRIOR FILING DATE: 1997-12-17
;; PRIOR APPLICATION NUMBER: 60/074,121
;; PRIOR FILING DATE: 1998-02-09
;; PRIOR APPLICATION NUMBER: 60/081,563
;; PRIOR FILING DATE: 1998-04-13
;; PRIOR APPLICATION NUMBER: 60/096,116
;; PRIOR FILING DATE: 1998-08-10
;; PRIOR APPLICATION NUMBER: 60/099,273

;; PRIOR FILING DATE: 1998-09-04
;; NUMBER OF SEQ ID NOS: 229
;; SOFTWARE: Patent.pm
;; SEQ ID NO 53
;; LENGTH: 500
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: sig_peptide
;; LOCATION: 199..288
;; OTHER INFORMATION: Von Heijne matrix
;; OTHER INFORMATION: score 5.5999990463257
;; NAME/KEY: polyA_signal
;; LOCATION: 464..469
;; NAME/KEY: polyA_site
;; LOCATION: 489..500
;; NAME/KEY: misc_feature
;; LOCATION: 197..412
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA429945
;; NAME/KEY: misc_feature
;; LOCATION: 61..195
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA429945
;; NAME/KEY: misc_feature
;; LOCATION: 197..412
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;; OTHER INFORMATION: id: W93646
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;; OTHER INFORMATION: id: W93646
;; NAME/KEY: misc_feature
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;; LOCATION: 90..195
;; OTHER INFORMATION: homology
;; OTHER INFORMATION: id: AA516431
;; NAME/KEY: misc_feature


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LOCATION: 425..488
OTHER INFORMATION: homology
OTHER INFORMATION: id :AA516431
OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 52..195
OTHER INFORMATION: homology
OTHER INFORMATION: id :W38899
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OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 197..338
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OTHER INFORMATION: id :W52820
OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 71..195
OTHER INFORMATION: homology
OTHER INFORMATION: id :W52820
OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 339..401
OTHER INFORMATION: homology
OTHER INFORMATION: id :W52820
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OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 40..195
OTHER INFORMATION: homology
OTHER INFORMATION: id :W19506
OTHER INFORMATION: est
NAME/KEY: misc feature
LOCATION: 9..10,12
OTHER INFORMATION: n=a, g, c or t
US-09-663-600A-53

Alignment Scores:
Pred. No.: 2,056-63
Score: 489.00
Percent Similarity: 98.00%
Best Local Similarity: 98.00%
Query Match: 96.26%
Length: 500
Matches: 98
Conservative: 0
Mismatch: 1
Indels: 1
Gaps: 0

US-09-801-115B-2 (1-99) x US-09-663-600A-53 (1-500)
Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIysGlyHis 20
Db 132 ATGATTAACGTGCAGCCGAAATTAACATCGCCCTCTCTCAGTGTAAGGCGAC 191
Qy 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuI 40
Db 192 GTGAGAGATGCTGGCGGTGATATTATCACTGATTAACAACAGATTATCATGCTCAT 251
Qy 40 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 252 CGTATCTGTGTGGCACTGATACCAAGAAACCAACATTTGACAGTTGGAGGGGTGTT 311
Qy 60 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
Db 60 ATTATCACTCACTGATTAACAACAGATTATCATGCTCATCTATCTGTGTGGCACTGATA 439
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Db 312 TGCACTTGACAGCAATATCTGTCTGCCACAGGGGCCCTTATTTACCGAAGCTTC 371
Qy 80 uphAsnProSerGlyProTyrGlnLysLysProValHisGluLysGlyValLeu 99
Db 372 GTTCATCCCAAGGGGTCTTACCAAGAAAAAGCTGTGATGAAAAAAGAAATTTTG 429

RESULT 7
US-09-599-360B-70
Sequence 70, Application US/09599360B
Patent No. 654863
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: GENSET 0500C3
CURRENT APPLICATION NUMBER: US/09/599,360B
CURRENT FILING DATE: 2000-06-21
PRIOR APPLICATION NUMBER: 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/141,032
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 09/469,099
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patent.pm
SEQ ID NO 70
LENGTH: 669
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 140..595
NAME/KEY: sig peptide
LOCATION: 140..442
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 4.10
NAME/KEY: polyA signal
LOCATION: 630..635
NAME/KEY: polyA site
LOCATION: 655..669
US-09-599-360B-70

Alignment Scores:
Pred. No.: 1,266-60
Score: 471.50
Percent Similarity: 65.13%
Best Local Similarity: 92.81%
Query Match: 4
Length: 669
Matches: 99
Conservative: 0
Mismatch: 53
Indels: 1
Gaps: 1

US-09-801-115B-2 (1-99) x US-09-599-360B-70 (1-669)
Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValIysGlyHis 20
Db 140 ATGATTAACGTGCAGCCGAAATTAACATCGCCCTCTCTCAGTGTAAGGCGAC 139
Qy 21 ValLysMetLeuArg----- 25
Db 200 GTGAGAGATGCTGGCGGTGACATACTGATGACATTTATTTATCATCGACAA 259
Qy 25 ----- 25
Db 260 GCCCGTAACCATATTATTGTTATCATCTGATTGAAGTCAACCGTTATCTTATTTTCATA 319
Qy 26 -----LeuAsp 27
Db 320 CTTTATATGTAATCACTGATTCATTAATGAAGTGTATTATTTGGCTTGTGAT 379
Qy 28 IleIleAsnSerLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
Db 380 ATTATCACTCACTGATTAACAACAGATTATCATGCTCATCTATCTGTGTGGCACTGATA 439
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Qy 48 ProglutrhtrhrleuthrValGlyGlyValPheAlaLeuValThrAlaCys 67
Db 440 CCAAGAACACAACTTACAGTGTGTGAGGGGTTTTCACCTTGACAGCAGTATGC 499
Qy 68 CysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGlyProTyr 87
Db 500 TGTCTTGGCCGAGCGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCACGCGGCTTAC 559
Qy 88 GlnLysLysProValHisGlnLysGlyGlyValLeu 99
Db 560 CAGAAAGCCTGTGCATGAAAAAAGAAAGTTTGG 595
RESULT 8
US-09-385-982-95
; Sequence 95, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCNDA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 95
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(392)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-95
Alignment Scores:
Pred. No.: 5.73e-44 Length: 392
Score: 357.00 Matches: 71
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.28% Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x US-09-385-982-95 (1-392)
Qy 26 LeuAspIleIleAsnSerLeuValThrValPheMetLeuIleValSerValLeuAla 45
Db 44 CTGTATATTATCACTCACTGTAACACAGTATTCATGCTCATGCTGTTGGCA 103
Qy 46 LeuIleProGluThrThrThrThrValGlyGlyGlyValPheAlaLeuValThrAla 65
Db 104 CTGATACCAAGAACACAACTTGACAGTGTGTGAGGGGTTTTCACCTTGTAACA 163
Qy 66 ValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSerGly 85
Db 164 GTATCTCTCTTGGCGAGCGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCACGCGGT 223
Qy 86 ProTyrGlnLysLysProValHisGlnLysLys 96
Db 224 CTTTACCAAGAAAGCCTGTGCATGAAAAA 256
RESULT 9
US-09-251-645-11
; Sequence 11, Application US/09251645
; Patent No. 6281413
; GENERAL INFORMATION:

APPLICANT: Kramer, Vance C.
APPLICANT: Morgan, Michael K.
APPLICANT: Anderson, Arne R.
APPLICANT: Hart, Hope
APPLICANT: Warren, Gregory W.
APPLICANT: Dunn, Martha
APPLICANT: Chen, Jeng S.
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
FILE REFERENCE: CGC1963/A
CURRENT APPLICATION NUMBER: US/09/251,645
CURRENT FILING DATE: 1999-02-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 37948
TYPE: DNA
ORGANISM: Photorhabdus luminescens
FEATURE:
NAME/KEY: CDS
LOCATION: (15171)..(18035)
OTHER INFORMATION: orf5
FEATURE:
NAME/KEY: CDS
LOCATION: (23768)..(31336)
OTHER INFORMATION: hph2
FEATURE:
NAME/KEY: CDS
LOCATION: (31393)..(35838)
OTHER INFORMATION: orf2
US-09-251-645-11
Alignment Scores:
Pred. No.: 2.47 Length: 37948
Score: 83.00 Matches: 28
Percent Similarity: 51.76% Conservative: 16
Best Local Similarity: 32.94% Mismatches: 21
Query Match: 16.34% Indels: 20
Gaps: 5
US-09-801-115B-2 (1-99) x US-09-251-645-11 (1-37948)
Qy 12 ProPheCysPheSerValLysGlyHisValLysMetLeuArgLeuAspIleIleAsnSer 31
Db 6476 CCAATATGCTTCTTAAGAAATGACACCTGAATATCAAAACCTTATTAACAGT 6535
Qy 32 LeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThrThr 51
Db 6536 TTGATTA---CTAATGATATTATGTTGCTCAATATGCTATGCAAGAAAGCTACGAAA 6589
Qy 52 ThrLeu-----ThrValGlyGlyGlyValPheAlaLeuValThrAla 65
Db 6590 TCCCTTCATGATTAATAGTAATACGCTTATATGCGGAGATGGCTATC-----TGA 6643
Qy 66 ValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSer--- 84
Db 6644 GTATGGGTATGCGCGAA-----ATATTACGACCATCAAAAC 6679
Qy 85 ---GlyProTyrGln 88
Db 6680 TGAAGTCCATCATCAG 6694
RESULT 10
US-09-116-498-11
; Sequence 11, Application US/09116498
; Patent No. 6251582
; GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
Deng, Hongkui
Unutmaz, Derya
Ramanul, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF

IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-343-1684
TELEFAX: 201-487-5800
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ORGANISM: pigtail macaque
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-116-498-11
Alignment Scores:
Pred. No.: 0.387 Length: 1083
Score: 73.00 Matches: 25
Percent Similarity: 39.33% Conservative: 10
Best Local Similarity: 28.09% Mismatches: 24
Query Match: 14.37% Indels: 30
DB: 3 Gaps: 4
US-09-801-115B-2 (1-99) x US-09-116-498-11 (1-1083)
QY 8 11eleYsh1aRgProPhCySPhSeSeVallySgLyH1sVallySmetLeuAArgLeuAasp 27
DB 529 ATTGATGATAGGCACTACTGT-----GCAAGAGAAAAGGCACTCCCACTTAA 576
QY 28 11ele1aSeSerLeuValThrThrValPheMetLeu1eValSerValLeuAlaLeu1le 47
DB 577 CTCATATGCGCCCTGCGCTTAATTTCACCTTTTGTCCCTTTGTTG----- 627
QY 48 ProGluThrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThralaValCys 67
DB 628 -----AGCATGTGACCTGCTACTGT 648
QY 68 CyeLeuAlaSpGlyAlaLeu1leTyRArgLySeuLeuPheAnProSeGlyProTyR 87
DB 649 TGCATTGCA-----AGGAGCTGTGTGCCAT-----TAC 678
QY 88 GlnLySlySProValHisGlyLySlys 96
DB 679 CAGCAGTCAGGAGACACACAAAAG 705
RESULT 11
US-09-170-496D-179
Sequence 179, Application US/09170496D

Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Law, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
SOFTWARE: Patent version 3.1
SEQ ID NO 179
LENGTH: 1083
TYPE: DNA
ORGANISM: Homo sapiens
US-09-170-496D-179
Alignment Scores:
Pred. No.: 0.387 Length: 1083
Score: 73.00 Matches: 25
Percent Similarity: 39.56% Conservative: 11
Best Local Similarity: 27.47% Mismatches: 27
Query Match: 14.37% Indels: 28
DB: 4 Gaps: 4
US-09-801-115B-2 (1-99) x US-09-170-496D-179 (1-1083)
QY 8 11eleYsh1aRgProPhCySPhSeSeVallySgLyH1sVallySmetLeuAArgLeuAasp 27
DB 529 ATTGATGATAGGCACTACTGT-----GCAAGAGAAAAGGCACTCCCACTTAA 576
QY 28 11ele1aSeSerLeuValThrThrValPheMetLeu1eValSerValLeuAlaLeu1le 47
DB 577 CTCATATGCGCCCTGCGCTTAATTTCACCTTTTGTCCCTTTGTTG----- 627
QY 48 ProGluThrThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThralaValCys 67
DB 628 -----AGCATGTGACCTGCTACTGT 648
QY 68 CyeLeuAlaSpGlyAlaLeu1leTyRArgLySeuLeu-----PheAnProSeGly 85
DB 649 TGCATTGCA-----AGGAGCTGTGTGCCATTCAGCAATCAGGA 690
QY 86 ProTyRGlnLySProValHisGlyLySlys 96
DB 691 AAGCACACAAAAGCTGAAGAAATCTTAGAAG 723
RESULT 12
US-09-116-498-7
Sequence 7, Application US/09116498
Patent No. 6251582
GENERAL INFORMATION:
APPLICANT: Littleman, Dan R.
Deng, Hongkui
Unutemaz, Derya
Ramani, Vineet N.K.
TITLE OF INVENTION: NOVEL ALTERNATIVE G-COUPLED RECEPTORS
ASSOCIATED WITH RETROVIRAL ENTRY INTO CELLS, METHODS OF
IDENTIFYING THE SAME, AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/116,498
FILING DATE: 16-Jul-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-116-498-7

Alignment Scores:
Pred. No.: 0.766 Length: 1083
Score: 71.00 Matches: 24
Percent Similarity: 39.33% Conservative: 11
Best Local Similarity: 26.97% Mismatches: 24
Query Match: 13.98% Indels: 30
Gaps: 4

US-09-801-115b-2 (1-99) x US-09-116-498-7 (1-1083)

QY 8 ILEYSHSARGPROPHCYSPHESERVALYSGLYHSVALYMETLEARGLEUASP 27
DB 529 ATTGATGATAGCCATCTGT-----GCAGAGAAAAGCACAATCCCAATTAA 576
QY 28 ILELEANSERLEUVALTHTRVALPHEMETLEUVALSERVALLEUALALEU 47
DB 577 CTCATATGTCCTGGTGCCCTTAATTTCACCTTTTGTCCCTTGTTG----- 627
QY 48 PROGLUTHRTHRTHLEUTHRVALIGLYGYVALPHEALALEUVALTHRALAVALCY 67
DB 628 -----ACGATTGTGACCTGCTACTGT 648
QY 68 CYSLEUALASPGLYALALEUILETYRARGLYSLEULEUPHEANPROSERGYPROTYR 87
DB 649 TGCATTGCA-----AGGAAGCTGTGTGCCAT-----TAC 678
QY 88 GLNLYSPROVALHISGLULYLYS 96
DB 679 CAGCAATCAGAGAAAGCACAACAAAAG 705

RESULT 13
US-09-170-496D-27
Sequence 27, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09/170,496D
CURRENT FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294
SOFTWARE: Patentin version 3.1
SEQ ID NO 27
LENGTH: 1083

TYPE: DNA
ORGANISM: Homo sapiens
US-09-170-496D-27

Alignment Scores:
Pred. No.: 0.766 Length: 1083
Score: 71.00 Matches: 24
Percent Similarity: 39.33% Conservative: 11
Best Local Similarity: 26.97% Mismatches: 24
Query Match: 13.98% Indels: 30
Gaps: 4

US-09-801-115b-2 (1-99) x US-09-170-496D-27 (1-1083)

QY 8 ILEYSHSARGPROPHCYSPHESERVALYSGLYHSVALYMETLEARGLEUASP 27
DB 529 ATTGATGATAGCCATCTGT-----GCAGAGAAAAGCACAATCCCAATTAA 576
QY 28 ILELEANSERLEUVALTHTRVALPHEMETLEUVALSERVALLEUALALEU 47
DB 577 CTCATATGTCCTGGTGCCCTTAATTTCACCTTTTGTCCCTTGTTG----- 627
QY 48 PROGLUTHRTHRTHLEUTHRVALIGLYGYVALPHEALALEUVALTHRALAVALCY 67
DB 628 -----ACGATTGTGACCTGCTACTGT 648
QY 68 CYSLEUALASPGLYALALEUILETYRARGLYSLEULEUPHEANPROSERGYPROTYR 87
DB 649 TGCATTGCA-----AGGAAGCTGTGTGCCAT-----TAC 678
QY 88 GLNLYSPROVALHISGLULYLYS 96
DB 679 CAGCAATCAGAGAAAGCACAACAAAAG 705

RESULT 14
US-09-016-434-1079
Sequence 1079, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Setlamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1079:
SEQUENCE CHARACTERISTICS:

LENGTH: 1232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1171145
US-09-016-434-1079

Alignment Scores:
Pred. No.: 0.927 Length: 1232
Score: 71.00 Matches: 24
Percent Similarity: 39.33% Conservative: 11
Best Local Similarity: 26.97% Mismatches: 24
Query Match: 13.98% Indels: 30
Gaps: 4

US-09-801-115B-2 (1-99) x US-09-016-434-1079 (1-1232)

QY 8 llelshsargpPheCysPheSerValIysGlyHisValIysMetLeuArgLeuAsp 27
Db 611 ATTGATGATATAGCATCTCTG-----GCAGAGAAAAGCACTCCATTAA 658
QY 28 llelshsargpPheCysPheSerValIysGlyHisValIysMetLeuArgLeuAsp 47
Db 659 CTCATATGTCCTCGTGGCTTATTTTCACCTTTTGTCTTGTCTTGTG----- 709
QY 48 ProglutThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 67
Db 710 -----AGCATGTGACCTGCTACTGT 730
QY 68 CysLeuAlaaspGlyAlaLeuIleTyArgIysLeuLeuPheAsnProSerGlyProTyr 87
Db 731 TGCATTGCA-----AGCAAGCTGTGTGCCAT-----TAC 760
QY 88 GluIysLysProValHisGluLysLys 96
Db 761 CAGCAATCAGAAAGCACACAAAAG 787

RESULT 15
US-08-061-092A-2/c
Sequence 2, Application US/08061092A
Patent No. 5587458
GENERAL INFORMATION:
APPLICANT: KING, C R
APPLICANT: KASPRZYK, Philip G
TITLE OF INVENTION: BIRD, Robert E
TITLE OF INVENTION: ANTI-erbB-2 ANTIBODIES, COMBINATIONS
TITLE OF INVENTION: THEREOF, AND THERAPEUTIC AND DIAGNOSTIC USES THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/061.092A
FILING DATE: 14-MAY-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 018797-014
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..720
US-08-061-092A-2

Alignment Scores:
Pred. No.: 1.95 Length: 720
Score: 66.50 Matches: 22
Percent Similarity: 48.61% Conservative: 13
Best Local Similarity: 30.56% Mismatches: 20
Query Match: 13.09% Indels: 17
Gaps: 4

US-09-801-115B-2 (1-99) x US-08-061-092A-2 (1-720)

QY 28 llelshsargpPheCysPheSerValIysGlyHisValIysMetLeuArgLeuAsp 44
Db 684 GTAGTACATAGCATAGTAAAGCACTATATAGAGACACATATATAGCGCAGT 625
QY 45 AlaLeuIleProglutThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 62
Db 624 GTCTCAGATGTAGGCTGTGAGCTGAGAGTGAAGTGGCGCGTGGAGGA----- 577
QY 63 ValThrAlaValCysCysLeuAlaaspGlyAlaLeuIleTyArgLys 78
Db 576 -----TGCTCTGCTGTATATAGCTGCGCTTGGAGAAATTCGGGTGCATATACAGTATT 523
QY 79 -----LeuLeuPheAsnProSerGlyProTyrGln 88
Db 522 ACCATTCTCAGATGATGATTCATCCATTCATTCCAG 487

Search completed: January 31, 2004, 05:27:07
Job time : 89 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2004, 02:59:32 ; Search time 247 Seconds

(without alignments)
1081.961 Million cell updates/sec

Title: US-09-801-115B-2

Perfect score: 508
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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delpop 6.0 , Delpext 7.0	

Searched: 2552756 segs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seg length: 0

Maximum DB seg length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=N.Geneseq.150un3-QFWT=fastap-SUFFIX=p2n.rng-MINMATCH=0.1-DOOPCL=0
-LOOPEXT=0-UNITS=bits-START=1-END=-1-MATRIX=blos62-TRANS=human40.cdi
-LIST=45-DOCALLFN=200-THR SCORE=pct-THR MAX=100-THR MIN=0-ALIGN=15
-MODE=LOCAL-OUTFMT=pico-NORMext-HEAPSIZE=500-MINLEN=0-MAXLEN=200000000
-USER=US09801115@CGN_1_1_490@runat_30012004_113847_7015-NCPU=6-ICPU=3
-NO_MMAP-LARGEQUERY-NEG SCORES=0-WAIT-DSPBLOCK=100-IONGLOG
-DEV TIMEOUT=120-WARN TIMEOUT=30-THREADS=1-XGAPOP=10-XGAPEXT=0.5-FGAPOP=6
-FGAPEXT=7-YGAPOP=10-YGAPEXT=0.5-DELOP=6-DELEXT=7

Database :

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2: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
3: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
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11: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
12: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1990.DAT.*
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15: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1993.DAT.*
16: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1994.DAT.*
17: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1995.DAT.*
18: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1996.DAT.*
19: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1997.DAT.*
20: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1998.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA1999.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2000.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2001A.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseq-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
1	508	100.0	413	20	AAK97873	Human secreted pro
2	508	100.0	439	19	ABK36006	CDNA sequence #397
3	508	100.0	504	24	AAV59598	Human secreted pro
4	508	100.0	504	24	ABK73585	Human CDNA #1 for
5	508	100.0	506	19	AAV59746	Human secreted pro
6	508	100.0	506	24	ABK73739	Human CDNA #2 for
7	508	100.0	515	21	AAK87730	Human secreted pro
8	508	100.0	515	22	AAK64012	Human secreted pro
9	508	100.0	534	22	AAK38005	UCL-1 nucleotide s
10	508	100.0	538	22	AAH98515	Human EST-derived
11	508	100.0	538	22	AAH98548	Human EST-derived
12	508	100.0	558	22	AAH34835	Human colon cancer
13	508	100.0	655	22	AAK44932	CDNA encoding nove
14	504	99.2	297	21	AAK15919	Human protein clon
15	504	99.2	467	21	AAK15929	Human protein clon
16	489	96.3	500	20	AAK97826	Human secreted pro
17	471.5	92.8	459	21	AAK38007	UCL-2 nucleotide s
18	471.5	92.8	637	21	AAZ56747	Human transmembran
19	471.5	92.8	663	20	AAZ34051	Human PRO772 nucle
20	471.5	92.8	663	21	AAK78498	Human PRO772 (UNQ4
21	471.5	92.8	663	21	AAK58238	Human PRO772 nucle
22	471.5	92.8	663	25	ABK92423	CDNA encoding huma
23	471.5	92.8	669	21	AAK87771	Human secreted pro
24	471.5	92.8	669	22	AAK64053	CDNA encoding huma
25	471.5	92.8	670	24	ABK90366	Human polynucleoti
26	471.5	92.8	908	22	AAK44933	CDNA encoding nove
27	467.5	92.0	638	24	ABK35884	CDNA sequence #275
28	461	90.7	415	21	AAK00147	Human secreted pro
29	357	70.3	392	21	AAK16090	Human colon cancer
30	339.5	66.8	363	21	AAK38009	UCL-4 nucleotide s
31	339.5	66.8	566	22	AAK45120	CDNA encoding nove
32	339.5	66.8	566	22	AAK45121	CDNA encoding nove
33	331	65.2	204	21	AAK38008	UCL-3 nucleotide s
34	323	63.6	321	20	AAK97651	Extended human sec
35	318.5	62.7	495	20	AAK34509	Human EST DNA43509
36	318.5	62.7	495	21	AAK78499	Human EST DNA43509
37	318.5	62.7	495	22	AAK93358	CDNA encoding SRT
38	318.5	62.7	495	25	ABK92424	Human secreted pro
39	317	62.4	354	20	AAK41509	Human secreted pro
40	294	57.9	379	21	AAK41512	Human secreted exp
41	257.5	50.7	465	22	ABK09082	Human transmembran
42	245	48.2	207	24	ABK94246	Gene #744 used to
43	245	48.2	207	24	ABK62782	Breast cancer rela
44	245	48.2	207	24	ABK62959	Breast cancer rela
45	245	48.2	207	24	ABK63180	Breast cancer rela

ALIGNMENTS

RESULT 1
AAK97873
ID AAK97873 standard; CDNA, 413 BP.
XX
XX AAK97873;
XX
XX 23-SEP-1999 (first entry)
XX
XX Human secreted protein encoding CDNA #61.
XX
XX Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;
XX
XX diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX
XX Homo sapiens.
XX
XX WO925825-A2.
XX

PD 27-MAY-1999.
XX
PF 13-NOV-1998; 98MO-IB01862.
XX
PR 04-SEP-1998; 98US-0099273.
PR 13-NOV-1997; 97US-0066677.
PR 17-DEC-1997; 97US-0069957.
PR 09-FEB-1998; 98US-0074121.
PR 13-APR-1998; 98US-0081563.
PR 10-AUG-1998; 98US-0096116.
XX
PA (GEMT) GENSET.
XX
PI Bougueleret L, Duclet A, Dumas Milne Edwards J;
XX
DR WPI; 1999-347472/29.
DR P-PSDB; AAY36189.
XX
PT Extended cDNAs encoding secreted proteins
XX
PS Claim 1; Page 261; 307pp; English.
XX
CC AAX97813-X97906 represent extended cDNA's which encode novel human
CC secreted proteins (see AAY36129-136222) and which have cytotostatic,
CC thrombotic and osteopathic activity. The extended cDNAs can be used to
CC express secreted proteins or parts of them or to obtain antibodies
CC capable of binding to the secreted proteins. They may also be used in
CC diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC Uses also include design of expression vectors and secretion vectors.
XX
SQ Sequence 413 BP; 121 A; 82 C; 95 G; 115 T; 0 other;
XX
Alignment Scores:
Pred. No.: 5,46e-58 Length: 413
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-801-115B-2 (1-99) x AAX97873 (1-413)
QY 1 MetAspAsnValGlnProLysIleuYHisArgProPheCysPheSerVallySGlyHis 20
Db 46 ATGGATTAACGTCGACCGCAAAATTAACATCGCCCTTCTCTCAGTGTAAAGCCAC 105
QY 21 VallyMetLeuArgLeuAspIleleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 106 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTACACAGATATTATGCTCATC 165
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 166 GTATCTGTGTGGCATGATACCAAGAAACCAACATTGACATGTGGAGGGGTGTTT 225
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleYrArgLysLeuLeu 80
Db 226 GCACCTGTGACAGCAGATATGCTGCTGCGACGGGGCCCTTATTACCGGAAGCTTCTG 285
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGlyLysGlyValLeu 99
Db 286 TTCAATCCACGCGGTCTTACCAAGAAAGCTGTGATGATAAAAAAGAGTTTGG 342
RESULT 2
ID ABR36006 standard; cDNA; 439 BP.
XX ABR36006;
XX AC ABR36006;
XX
DT 08-MAY-2002 (first entry)
XX
XX cDNA sequence #397 encoding novel human secreted protein.
XX
XX Human secreted protein; hyperproliferative disorder; autoimmune disorder;

KW immune deficiency disorder; blood disorder; inflammatory disorder;
KW infectious disorder; allergic condition; neurodegenerative disorder;
KW liver fibrosis; coagulation disorder; gene therapy; antimicrobial;
KW tumour; cancer; hepatotropic; immunosuppressive; antineumatic; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200177289-A2.
XX
XX
XX 18-OCT-2001.
XX
XX 29-MAR-2001; 2001MO-US10232.
XX
XX 06-APR-2000; 2000US-195605P.
XX
XX (GEMT) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, Lavallie ER, Collins-Racie LA, Evans C;
PI Werberg D, Treacy M, Agostino MU, Bowman MR, Spaulding V, Wong GG;
PI Clark HF, Fechtel K, Howes SH, Resnick RJ, Gulkota K, Graham JR;
XX
XX WPI; 2002-179322/23.
XX
XX Six hundred and twenty three polynucleotides derived from a variety of
XX human tissue sources which encode secreted proteins, useful for
XX treating immune deficiencies and disorders such as autoimmune disorders
XX
PS Claim 1; Page 296-297; 393pp; English.
XX
XX The present invention relates to the isolation of novel cDNA sequences
XX which encode human secreted proteins. The cDNA sequences have been
XX derived from a variety of human tissues. The invention also provides
XX a method for producing proteins from these polynucleotide sequences.
XX The proteins are useful for identifying compounds that modulate their
XX activity and production. The sequences of the invention are
XX useful for treating diseases such as hyperproliferative disorders
XX (e.g. cancer), immune deficiency disorders (e.g. severe combined
XX immunodeficiency (SCID)), autoimmune disorders (e.g. multiple
XX sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory
XX disorders (e.g. arthritis), infectious disorders (e.g. hepatitis),
XX allergic conditions (e.g. asthma), neurodegenerative disorders (e.g.
XX Alzheimer's disease), liver fibrosis, coagulation disorders (e.g.
XX haemophilia), and tumours. The polynucleotide sequences of the
XX invention are also useful in gene therapy. ABR3610-ABR36232 represent
XX the cDNA sequences of the invention that encode for novel human
XX secreted proteins.
XX
SQ Sequence 439 BP; 117 A; 96 C; 104 G; 122 T; 0 other;
XX
Alignment Scores:
Pred. No.: 5,93e-58 Length: 439
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-801-115B-2 (1-99) x ABR36006 (1-439)
QY 1 MetAspAsnValGlnProLysIleuYHisArgProPheCysPheSerVallySGlyHis 20
Db 81 ATGGATTAACGTCGACCGCAAAATTAACATCGCCCTTCTCTCAGTGTAAAGCCAC 140
QY 21 VallyMetLeuArgLeuAspIleleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 141 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTACACAGATATTATGCTCATC 200
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 201 GTATCTGTGTGGCATGATACCAAGAAACCAACATTGACATGTGGAGGGGTGTTT 260
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleYrArgLysLeuLeu 80

DB 261 GCACTTGTGACAGAGATGCTGCTTGTCCGACGCGGCCCTTATTACCGAAGCTTCTG 320
QY 81 PheasnProSerGlyProTyrGlnIleValHisProValHisGluIleValIleu 99
DB 321 TTCAATCCGACGGCTCTTACCAAGAAAGCCTGTGATGAAAAAAGAGTTTGG 377
RESULT 3
AAV59598
ID AAV59598 standard; DNA; 504 BP.
XX AAV59598;
AC AAV59598;
XX 06-JAN-1999 (first entry)
DT
XX Human secreted protein gene 88 clone HAUAV32.
DE
XX Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
XX Homo sapiens.
OS
XX MO9839448-A2.
PN
XX 11-SEP-1998.
PD
XX 06-MAR-1998; 98WO-US04493.
PF
XX 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040336.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043668.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
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PR 23-MAY-1997; 97US-0047586.
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PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.

PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
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PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056633.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056642.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057669.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebnner R, Endress GA;
PI Feng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kwaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
XX WPI: 1998-506364/43.
XX P-FSDB; AAW74818.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological

PT disorders, immune diseases, inflammation or blood disorders
XX
PS Claim 1; Page 320; 721pp; English.
XX
CC This sequence represents a nucleic acid molecule designated Gene 88 from
CC the human cDNA clone HUVAV32 (deposited as clone ATCC 97901 and ATCC
CC 209047) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
CC the fused protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological conditions
CC can be diagnosed by determining the amount of the new polypeptides in a
CC sample or by determining the presence of mutations in the new
CC polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV59511 for described uses).
XX
SQ Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;
XX
Alignment Scores:
Pred. No.: 7.15e-58 Length: 504
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0
US-09-801-115B-2 (1-99) x AAV59598 (1-504)
QY 1 MetaspasnValGlnProLysIleLysHisArgProPheCysPheSerValIleGlyHis 20
Db 131 ATGCATTAACGCGCAGCCGAAATAAACAATGCCCCCTTCTGCTCAAGTGAAAGGCCAC 190
QY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 191 GTGAAGATGCTGCGCGTGGATATTATCACTCACTGGTAACACAGATTATCATCTCATC 250
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 251 GTACTGTGTGGACGATGATACCAAGAAACCAACATTGACAGTTGGGCGGTGTT 310
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspIleAlaLeuIleTyrArgLysLeuLeu 80
Db 311 GCACTTGTGACAGCAGATGCTGCTTCCGACCGGGCCCTTATTACCGAAGCTTCTG 370
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
Db 371 TTCATCCCAAGCGGTCTTACCAAGAAAGCGCTGTGATGAAAAAAGAGTTTGG 427
RESULT 4
ABST73585
ID ABST73585 standard; cDNA; 504 BP.
XX
AC ABST73585;
XX
DT 15-JAN-2003 (first entry)
XX
DE Human cDNA #1 for novel secreted protein gene 88.
XX
KW Human; 88; gene; secreted protein; autoimmune disease; chemotaxis;
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
KW cerebrovascular disorder; cerebral ischaemia; angiodysplasia; sunburn;
KW nervous system disorders; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing; tissue regeneration;
KW epithelial cell proliferation; organ transplantation; food additive;
KW preservative; nutritional.
XX
OS Homo sapiens.
XX

PN US6420526-B1.
XX
PD 16-JUL-2002.
XX
PE 08-SEP-1998; 98US-0149476.
XX
XX 07-MAR-1997; 97US-038621P.
XX 07-MAR-1997; 97US-040161P.
XX 07-MAR-1997; 97US-040162P.
XX 07-MAR-1997; 97US-040163P.
XX 07-MAR-1997; 97US-040333P.
XX 07-MAR-1997; 97US-040334P.
XX 07-MAR-1997; 97US-040336P.
XX 07-MAR-1997; 97US-040626P.
XX 11-APR-1997; 97US-043311P.
XX 11-APR-1997; 97US-043312P.
XX 11-APR-1997; 97US-043313P.
XX 11-APR-1997; 97US-043314P.
XX 11-APR-1997; 97US-043315P.
XX 11-APR-1997; 97US-043568P.
XX 11-APR-1997; 97US-043569P.
XX 11-APR-1997; 97US-043576P.
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XX 11-APR-1997; 97US-043659P.
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XX 11-APR-1997; 97US-043672P.
XX 11-APR-1997; 97US-043674P.
XX 23-MAY-1997; 97US-047492P.
XX 23-MAY-1997; 97US-047500P.
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XX 23-MAY-1997; 97US-047502P.
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XX 23-MAY-1997; 97US-047617P.
XX 23-MAY-1997; 97US-047618P.
XX 23-MAY-1997; 97US-047632P.
XX 23-MAY-1997; 97US-047633P.
XX 06-JUN-1997; 97US-048964P.
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XX 13-JUN-1997; 97US-049610P.
XX 08-JUL-1997; 97US-051928P.
XX 16-JUL-1997; 97US-052874P.
XX 18-AUG-1997; 97US-055724P.
XX 22-AUG-1997; 97US-056630P.
XX 22-AUG-1997; 97US-056631P.
XX 22-AUG-1997; 97US-056632P.
XX 22-AUG-1997; 97US-056636P.
XX 22-AUG-1997; 97US-056637P.

PR 22-AUG-1997; 97US-056662P.
PR 22-AUG-1997; 97US-056664P.
PR 22-AUG-1997; 97US-056845P.
PR 22-AUG-1997; 97US-056846P.
PR 22-AUG-1997; 97US-056862P.
PR 22-AUG-1997; 97US-056864P.
PR 22-AUG-1997; 97US-056872P.
PR 22-AUG-1997; 97US-056874P.
PR 22-AUG-1997; 97US-056875P.
PR 22-AUG-1997; 97US-056876P.
PR 22-AUG-1997; 97US-056877P.
PR 22-AUG-1997; 97US-056878P.
PR 22-AUG-1997; 97US-056879P.
PR 22-AUG-1997; 97US-056880P.
PR 22-AUG-1997; 97US-056881P.
PR 22-AUG-1997; 97US-056882P.
PR 22-AUG-1997; 97US-056884P.
PR 22-AUG-1997; 97US-056886P.
PR 22-AUG-1997; 97US-056887P.
PR 22-AUG-1997; 97US-056889P.
PR 22-AUG-1997; 97US-056890P.
PR 22-AUG-1997; 97US-056892P.
PR 22-AUG-1997; 97US-056893P.
PR 22-AUG-1997; 97US-056903P.
PR 22-AUG-1997; 97US-056908P.
PR 22-AUG-1997; 97US-056909P.
PR 22-AUG-1997; 97US-056910P.
PR 22-AUG-1997; 97US-056911P.
PR 22-AUG-1997; 97US-057616P.
PR 05-SEP-1997; 97US-057650P.
PR 05-SEP-1997; 97US-057669P.
PR 12-SEP-1997; 97US-058785P.
PR 02-OCT-1997; 97US-061060P.
PR 06-MAR-1998; 98MO-US04493.

(HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrrie AM;
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;

XX MPI; 2002-634796/68.
DR P-PDB; ABG95267.

PT New isolated human secreted protein for diagnosing, preventing,
PT treating or ameliorating medical conditions and used as a food additive
PT or preservative -

XX Example 1; SEQ ID No 98; 1299p; English.

CC The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of
CC 309 cDNA sequences also given in the specification. The protein is used
CC in a pharmaceutical composition used to prevent, treat or ameliorate a
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents a cDNA derived from a
CC gene encoding one of the novel human secreted proteins of the invention.
CC Note: This sequence did not form part of the printed specification,
CC but was obtained in electronic format directly from USPRO at

CC seqdata.uspto.gov/sequence.html?docID=6420526B1.

XX Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;

Alignment Scores:

Pred. No.:	7	156-58	Length:	504
Score:	508.00		Matches:	99
Percent Similarity:	100.00%		Conservative:	0
Best Local Similarity:	100.00%		Mismatches:	0
Query Match:	100.00%		Indels:	0
DB:	24		Gaps:	0

US-09-801-115B-2 (1-99) x AB873585 (1-504)

QY 1 MetaSpasnValGlnProlysilLeuYshisArpProPheCyPheSerValIlysgIyhis 20

Db 131 ATGGATTAACGTCACGCCGAAATTAACATCCCTTCTGCTTCAGTGTGAAGCCAC 190

QY 21 ValIyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40

Db 191 GTGAAGATGCTCGCGGCTGGATTTATTCACACTGCTGTAAACAAGTATTCATGCTCACC 250

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

Db 251 GATATCTGTGTGGCACTGATACCAAGAACACACATTACAGTGTGTGAGGGGTGTT 310

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArGlyLeuLeu 80

Db 311 GCACCTGTGACACAGCATATGCTGTCTTCCGACGGGGCCCTTATTTACCGAAGCTTCTG 370

QY 81 PheAsnProSerGlyProTyrGlnIlyslsProValHisGluIlyslsGluValLeu 99

Db 371 TTCATATCCACGCGGTCTTACAGAAACCCGTGTCATGAAGAAAAAGAGTTTG 427

RESULT 5

AAV59746

ID AAV59746 standard; DNA; 506 BP.

XX AAV59746;

XX 19-JUN-1999 (first entry)

XX Human secreted protein gene 88 clone HAAV32.

KM Human; secreted protein; fusion protein; gene therapy; protein therapy;

KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

KM developmental abnormality; foetal deficiency; blood; allergy; renal; ds;

KM immune system; aschma; lymphocytic disease; brain; hepatic; lymphoma;

KM inflammation; ischaemic shock; Alzheimer's disease; reastosis; AIDS;

KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;

KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;

KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.

OS Homo sapiens.

XX MO9839448-A2.

XX 11-SEP-1998.

XX 06-MAR-1998; 98MO-US04493.

XX 02-OCT-1997; 97US-0061060.

XX 07-MAR-1997; 97US-0038621.

XX 07-MAR-1997; 97US-0040161.

XX 07-MAR-1997; 97US-0040162.

XX 07-MAR-1997; 97US-0040163.

XX 07-MAR-1997; 97US-0040333.

XX 07-MAR-1997; 97US-0040334.

XX 07-MAR-1997; 97US-0040336.

XX 07-MAR-1997; 97US-0040626.

XX 11-APR-1997; 97US-0043311.

XX 11-APR-1997; 97US-0043312.

XX 11-APR-1997; 97US-0043313.

PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056633.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056864.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.

PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Feng P, Petrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
XX WPI; 1998-506364/43.
DR P-PSDB; AAW74961.
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1, Page 472; 72ipp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 88 from
CC the human cDNA clone HAUW32 (deposited as clone ATCC 97897 and ATCC
CC 209043) which encodes a secreted human protein. The gene can be used to
CC generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
CC the fused protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV59511 for described uses).
XX
XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;
SQ
Alignment Scores:
Pred. No.: 7,19e-58 Length: 506
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-801-115B-2 (1-99) x AAV59746 (1-506)
QY 1 MetAspAsnValAlaInProLySIIeLySHIAzPProPheCySPheSerValLySgIyHIs 20
Db 117 ATGATTAACGTCGACGCGAAATTAACATCCGCCCTTCGCTTCAGTGGAAAGCCAC 176
QY 21 ValLyMeIleuArgLeuaspIleIleasSerLeuValThrThraIphMeIleuIle 40
Db 177 GTAAGATGCTGGCGGTATTAATCACTCACTGTAACAACAGATTCATGTCATC 236
QY 41 ValSerValLeuAlaLeuIleProGIuTnThrThrLeuThrValSgIyGIyValPhe 60
Db 237 GTATCTGTGTGGCACTGATACCAAGAACACAACTTGACTGTGTGGAGGGGTGTT 296
QY 61 AlaLeuValThraIaValCysCysLeuAlaAepGIyAlaLeuIleTyzArgLySLeuLeu 80

PT treating or ameliorating medical conditions and used as a food additive
PT or preservative -

PS Example 1; SEQ ID No 252; 129pp; English.

CC The invention relates to an isolated protein that is one of 186 human
CC secreted proteins, given in the specification, encoded by one of
CC 309 cDNA sequences also given in the specification. The protein is used
CC in a pharmaceutical composition used to prevent, treat or ameliorate a
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
CC infections caused by bacteria, viruses and fungi and ocular disorders
CC e.g. corneal infection. The polypeptides can also be used to aid wound
CC healing and epithelial cell proliferation, to prevent skin aging due to
CC sunburn, to maintain organs before transplantation, for supporting cell
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
CC polypeptides can also be used as a food additive or preservative to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrate, vitamins, minerals, cofactors and other nutritional
CC components. The present sequence represents a cDNA derived from a
CC gene encoding one of the novel human secreted proteins of the invention.
CC Note: This sequence did not form part of the printed specification,
CC but was obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=6420526b1.

XX Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;

Alignment Scores:

Pred. No.:	7.19e-58	Length:	506
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-801-115B-2 (1-99) x ABS73739 (1-506)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVallyGlyHis 20
DB 117 ATGATTAACGTCGACCGCAAAATTAACATCGCCCTTCTGCTTCAAGTGTAAGGCCAC 176
QY 21 VallyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 177 GTGAAGATGTCGGCGCTGGATATTATCACTCACTGGTAACAACAGATATTATCTCATC 236
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 237 GTATCTGTGTTGGACATGATACAGAAACCAACATTTGAGTTGGAGGGGTGTTT 296
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
DB 297 GCACCTGTGAACAGAGATATGCTGCTTGGCCAGCGGGCCCTTATTATCCGGAACCTCTG 356
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGlyLysGluValLeu 99
DB 357 TTCAATCCACAGCGGTCTTACCAAAAAAGCTGTGATGAAAAAAGAGTTTG 413

RESULT 7

AAA87730 standard; cDNA; 515 BP.

XX AAA87730;

XX 28-NOV-2000 (first entry)

DE Human secreted protein encoding cDNA SEQ ID #29.

XX Human; secreted protein; forensic procedure; gene therapy;
KM chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;

KM cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KM brain disorder; skeletal muscle disorder; eye disorder; obesity;
KM mitochondrialcytopathy; diabetes; atherosclerosis; Alzheimer's disease;
KM neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KM septic shock; impotence; ss.

XX Homo sapiens.

XX WO200037491-A2.

XX 29-JUN-2000.

PF 20-DEC-1999; 99WO-IB02058.

XX 22-DEC-1998; 98US-0113686.

PR 25-JUN-1999; 99US-0141032.

XX (GEST) GENSET.

PI Bougueleret L, Dumas J, Duclert A;

DR WPI; 2000-442637/38.

DR P-PSDB; AAB25768.

PT Polynucleotides and polypeptides encoding proteins with signal
PT peptides, useful in diagnostic, forensic, gene therapy and chromosome
PT mapping procedures -

XX Claim 1; Page 169-170; 306pp; English.

XX This sequence represents human cDNA encoding a secreted protein. The
CC invention relates to sequences AAA87725-AA87774 which encode human
CC secreted proteins AAB25763-B25812. The proteins include signal peptides.
CC Included in the invention are a host cell containing one of the cDNA
CC sequences, and a purified antibody capable of binding to one of the
CC secreted proteins. Also contained in the invention are methods for
CC storing the sequence data on a computer system, and a method for
CC identifying features of the cDNA sequences using a computer programme.
CC The cDNAs are useful for expressing secreted proteins or fragments to
CC obtain antibodies capable of specifically binding to the secreted
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
CC therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondrialcytopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence.

XX Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Alignment Scores:

Pred. No.:	7.36e-58	Length:	515
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
		Gaps:	0

US-09-801-115B-2 (1-99) x AAA87730 (1-515)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVallyGlyHis 20

DB 144 ATGATTAACGTCGACCGCAAAATTAACATCGCCCTTCTGCTTCAAGTGTAAGGCCAC 203

QY 21 VallyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

DB 204 GTGAAGATGTCGGCGCTGGATATTATCACTCACTGGTAACAACAGATATTATCTCATC 263

QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

DB 264 GTATCTGTGTTGGACATGATACAGAAACCAACATTTGAGTTGGAGGGGTGTTT 323

```
QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 324 GCACCTGTGACAGACAGATGCTGCTTGGCCGAGGGCCCTTATTACCGGAAGCTTCG 383
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGlnLysGluValLeu 99
DB 384 TTCAAATCCAGCGCTCTTACGAAAAAGCCCTGTGCATGAAAAAAGAGTTTGG 440

RESULT 8
AAF64012
ID AAF64012 standard; cDNA; 515 BP.
XX
AC AAF64012;
XX
DT 05-APR-2001 (first entry)
XX
DE cDNA encoding human secreted protein #13.
XX
KW Secreted protein; prevention; treatment; diagnosis; disease;
XX infection; ds.
XX
OS Homo sapiens.
XX
PN MO200100806-A2.
XX
PD 04-JAN-2001.
XX
PF 21-JUN-2000; 2000MO-IB00951.
XX
PR 25-JUN-1999; 99US-0141032.
XX
PR 21-DEC-1999; 99US-0469099.
XX
PA (GEST ) GENSET.
XX
PI Dumas Malne Edwards J, Bougueleret L, Joberet S;
XX
DR WPI; 2001-071487/08.
XX
PT 49 Secreted proteins and the nucleic acids encoding them, useful in
XX gene therapy and for detecting similar sequences in samples -
XX
PS Claim 1; Page 225; 307pp; English.
XX
CC The present invention relates to 49 Secreted proteins and the cDNAs
XX encoding them. The protein and nucleic acids may be used in the
XX prevention, treatment and diagnosis of diseases associated with
XX inappropriate protein expression.
XX
SQ Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Alignment Scores:
Pred. No.: 7.36e-58 Length: 515
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAF64012 (1-515)
QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 144 ATGGATTAACGTGCGAGCCGAAAAATTAACATCGCCCTTGGCTTCACTGTGAAGGCCAC 203
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
DB 204 GTGAAGATGCTGGCGCTGGATATATCATCACTGATGAACAACAGATTCAATCATC 263
QY 41 ValSerValLeuAlaLeuIleProGlnThrThrThrThrValHisGlyGlyValPhe 60
DB 264 GTATCTGTGTGGCATGATACCAAGAAACCAACCAATGACATTGATGGAGGGGTGTTT 323
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```
QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
DB 324 GCACCTGTGACAGACAGATGCTGCTTGGCCGAGGGCCCTTATTACCGGAAGCTTCG 383
QY 81 PheAsnProSerGlyProTyrGlnLysProValHisGlnLysGluValLeu 99
DB 384 TTCAAATCCAGCGCTCTTACGAAAAAGCCCTGTGCATGAAAAAAGAGTTTGG 440

RESULT 9
AAA38006
ID AAA38006 standard; cDNA; 534 BP.
XX
AC AAA38006;
XX
DT 22-AUG-2000 (first entry)
XX
DE UCK-1 nucleotide sequence.
XX
KW UCK-1; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
XX radiotherapy; chemotherapy; human; ss.
XX
OS Homo sapiens.
XX
PN CN1244584-A.
XX
PD 16-FEB-2000.
XX
PF 14-MAY-1999; 99CN-0107284.
XX
PR 14-MAY-1999; 99CN-0107284.
XX
PA (UYBB-) UNIV BEIJING MEDICAL.
XX
PI Ma D, Han W, Zhang Y;
XX
DR WPI; 2000-388170/34.
XX
DR P-PSDB; AAY98142.
XX
PT Chemotactic factor useful for treatment and diagnosis of immunocyte
XX disorders - has immunocyte chemotactic stimulating factor
XX
PS Example 4; Fig 1; 31pp; Chinese.
XX
CC This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis
XX factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis
XX activity and a haemopoiesis stimulating effect. The invention relates to
XX UCK proteins, their encoding nucleotide sequences and antibodies and
XX antagonists against the proteins. The nucleotide and protein sequences
XX are useful for the preparation of a composition for the diagnosis and
XX treatment of diseases associated with abnormal immunocyte function and
XX low haemopoiesis function caused by radiotherapy and chemotherapy used to
XX treat tumours and other diseases.
XX
SQ Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;

Alignment Scores:
Pred. No.: 7.73e-58 Length: 534
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-801-115B-2 (1-99) x AAA38006 (1-534)
QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 152 ATGGATTAACGTGCGAGCCGAAAAATTAACATCGCCCTTGGCTTCACTGTGAAGGCCAC 211
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
DB 212 GTGAAGATGCTGGCGCTGGATATATCACTCACTGTGAACAACAGATTCAATCATC 271
```

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Qy 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 272 GTATCTGTGTGGACGATACGAGAAACCAACATTCAGTGTGGAGGGGCTGTTT 331
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
Db 332 GCACCTGTGACAGCAGATGCTGTCTGGCCGACGGGGCCCTTATTATCCGGAACCTTCTG 391
Qy 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValIleu 99
Db 392 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAAAAGAAAGTTTGG 448

RESULT 10
AAH98515/c
ID AAH98515 standard; cDNA; 538 BP.
XX
AC AAH98515;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 372.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001MO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dermanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR P-PSDB; AAM23856.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 451; 1275bp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

Alignment Scores:
Pred. No.: 7,81e-58 Length: 538
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAH98515 (1-538)
```

```
Qy 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlnHis 20
Db 366 ATGATACAGTCGACGCGGAAATATTAACATCCGCCCTTCTGCTTCAGTGGAAGGCCAC 307
Qy 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 306 GTGAGATGTGTGGCGGTGGATATTCAACTCACTGGTAAACAACATATTCAGCTTCATC 247
Qy 41 ValSerValIleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 246 GTATCTGTGTGGACCTGATACCAAGAACCAACATTCAGTGTGTGAGGGGCTGTTT 187
Qy 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
Db 186 GCACCTGTGACAGCAGATGCTGTCTGGCCGACGGGGCCCTTATTATCCGGAAGCTTCTG 127
Qy 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValIleu 99
Db 126 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAAAAGAAAGTTTGG 70

RESULT 11
AAH98548/c
ID AAH98548 standard; cDNA; 538 BP.
XX
AC AAH98548;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST-derived coding sequence SEQ ID NO: 405.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder;
KW biodiversity; gene therapy; nutrition; ss.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001MO-US02687.
XX
PR 25-JAN-2000; 2000US-0491404.
PR 17-JUL-2000; 2000US-0617746.
PR 03-AUG-2000; 2000US-0631451.
PR 15-SEP-2000; 2000US-0663870.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Dermanac RA, Zhang J, Werhman T;
XX
DR WPI: 2001-476164/51.
DR P-PSDB; AAM23889.
XX
PT Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use -
XX
PS Claim 1; Page 467; 1275bp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a cDNA
CC of the invention.
XX
SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;
```


Alignment Scores:
Pred. No.: 7,81e-58 Length: 538
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAH98548 (1-538)

QY 1 MetAspAsnValGlnProIlySileYshIArgProPheCysePheSerValIlysgIYhIs 20
Db 366 ATGGATTAACGTGACGCGGAAATTAACATCGCCCTTGCTTCAGTGGAAAGGCAC 307
QY 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 306 GTGAAGATGTGGCGCTGGATATTAATCACTGCTGTAACAACAGATTCAAGCTCATT 247
QY 41 ValSerValIleuAlaIleuIleProGluThrThrThreIeuThValGlyIyValPhe 60
Db 246 GTATCTGTGTGGACATGATACCAAGAAACCAACATTGACGTTGGTGGAGGGGTGTTT 187
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyraGlyIleu 80
Db 186 GCACCTGTGACACAGATGCTGTCTTGGCCGACGGGGCCCTTATTACCGGAAGCTTCTG 127
QY 81 PheAsnProSerGlyProTyrgInIlySProValHisGluIlySgluValIleu 99
Db 126 TTCATATCCACGGCGTCTTACAGAAAAGCCTGTGCATGAAAAAAGAGTTTGG 70

RESULT 12
AAH34835
ID AAH34835 standard; cDNA; 558 BP.
XX
AC AAH34835;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1917.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; ss.
XX
OS Homo sapiens.
XX
PN MO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000MO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
PR 03-NOV-1999; 99US-0163280.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI, 2001-235357/24.
XX
DR P-PSDB; AAG75430.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
PS Claim 1; Page 3428; 9803pp; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in the prevention,
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders

CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing
CC inactive proteins or to supplement the patient's own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps,
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;

Alignment Scores:
Pred. No.: 8,21e-58 Length: 558
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 22 Gaps: 0

US-09-801-115B-2 (1-99) x AAH34835 (1-558)

QY 1 MetAspAsnValGlnProIlySileYshIArgProPheCysePheSerValIlysgIYhIs 20
Db 147 ATGGATTAACGTGACGCGGAAATTAACATCGCCCTTGCTTCAGTGGAAAGGCAC 206
QY 21 ValIlyMetLeuArgLeuAspIleIleAsnSerLeuValThrValPheMetLeuIle 40
Db 207 GTGAAGATGTGGCGCTGGATATTAATCACTGCTGTAACAACAGATTCAAGCTCATT 266
QY 41 ValSerValIleuAlaIleuIleProGluThrThrThreIeuThValGlyIyValPhe 60
Db 267 GTATCTGTGTGGACATGATACCAAGAAACCAACATTGACGTTGGTGGAGGGGTGTTT 326
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyraGlyIleu 80
Db 327 GCACCTGTGACACAGATGCTGTCTTGGCCGACGGGGCCCTTATTACCGGAAGCTTCTG 386
QY 81 PheAsnProSerGlyProTyrgInIlySProValHisGluIlySgluValIleu 99
Db 387 TTCATATCCACGGCGTCTTACAGAAAAGCCTGTGCATGAAAAAAGAGTTTGG 443

RESULT 13
AAS44932
ID AAS44932 standard; cDNA; 655 BP.
XX
AC AAS44932;
XX
DT 18-DEC-2001 (first entry)
XX
DE cDNA encoding novel human secretory protein, Seq ID No 13.
XX
XX Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
XX ischemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
XX transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
XX amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
XX ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
XX gut protection; lung; liver fibrosis; immune deficiency; infection;
XX severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
XX multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
XX fertility; analgesic; pain; antigen; ss.
XX
OS Homo sapiens.
XX
PN MO200166689-A2.
XX
PD 13-SEP-2001.
XX
PF 05-MAR-2001; 2001MO-US04942.
XX

PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSEQ-) HYSEQ INC.
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX WPI; 2001-589934/66.
 DR P-PSDB; AAU28032.
 XX
 PT Novel polypeptides and nucleic acids obtained from cDNA libraries
 PT prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 PS
 PS Claim 1; SEQ ID No 13; 107bp; English.
 XX
 CC The invention relates to novel isolated human secreted polypeptides (I)
 CC and polynucleotides (II). (I) and (II) are useful for treating
 CC inflammatory conditions such as arthritis, nephritis, Crohn's disease,
 CC ischaemia-reperfusion injury, shock, sepsis, immune responses, and is
 CC involved in increasing haematopoiesis, stem cell survival, bone growth
 CC and remodeling. (I), (II) and modulators of (II) are useful for
 CC prophylaxis or treatment of one or more cancers. (II) is also useful for
 CC creating transgenic animals useful for studying the in vivo activities of
 CC the polypeptide as well as for studying modulators of the polypeptides.
 CC (I) induces the proliferation of neural cells and regeneration of nerve
 CC and brain tissue and is useful for the treatment of central and
 CC peripheral nervous system diseases and neuropathies, such as Alzheimer's,
 CC Parkinson's disease, Huntington's disease, and amyotrophic lateral
 CC sclerosis. In addition, (I) is involved in chemotactic or chemokinetic
 CC activity, regulation of haematopoiesis and is useful for treating myeloid
 CC or lymphoid cell disorders, platelet disorders such as thrombocytopenia
 CC and for regeneration of bone, cartilage, tendon, ligament and/or nerve
 CC tissue growth, and in tissue repair, healing of burns, incisions,
 CC ulcers, for treating osteoporosis, osteoarthritis, bone degenerative
 CC disorders, or periodontal disease. Furthermore, (I) is also useful for
 CC gut protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues, various immune deficiencies and
 CC disorders including severe combined immunodeficiency (SCID), bacterial or
 CC fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic
 CC reactions and conditions, such as asthma or other respiratory problems.
 CC In addition, (I) affects biorhythms or circadian cycles of rhythms,
 CC fertility, metabolism, catabolism, anabolism, storage or elimination of
 CC dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides
 CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.
 CC
 XX
 XX Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;
 XX
 XX
 Alignment Scores:
 Pred. No.: 1.02e-57 Length: 655
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0
 US-09-801-115B-2 (1-99) x AAS44932 (1-655)
 QY 1 MetaspamValGlnPolysIILyGHIARProPhCySPhesValIyGlyHis 20
 DB 134 ATGGATTAACGGCGACCGCAAAATAAACATCGCCCTTCCTCAGTGGAAAGGCGCAC 193
 QY 21 ValIyMetLeuAAGLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

DB 194 GTGAGATGCTGGCGGTGGATATATCACTGACGTAAACAACAGTATTCATGCTCATC 253
 QY 41 ValSerValIleuAlaIleuIleProGluThrThrThLeuThyValGlyGlyValIlePhe 60
 DB 254 GTATCTGTGTGGCACTGATACCGAAACCAACACTTACACTTGTGGAGGGGTGTTT 313
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaIleuIleTyrArgIyLeuLeu 80
 DB 314 GCACCTGTGACACAGCATATGCTGTCTTGGCAGCGGGCCCTTATTTAACCGAAGCTTCTG 373
 QY 81 PheAsnProSerGlyProTyrGlnIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 99
 DB 374 TTCAATCCAGCGGTCTTACCGAAGAAAGCCGTGTCATGAAAAAGAAAGATTITG 430
 RESULT 14
 ID AAA15919 standard; cDNA; 297 BP.
 AC AAA15919;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Human protein clone HP10357 coding sequence.
 XX
 XX Human protein; hydrophobic domain; nutritional source; haematopoiesis;
 KW cytokine production; cell proliferation; cell differentiation;
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 MO200005367-A2.
 XX
 PD 03-FEB-2000.
 XX
 PF 22-JUL-1999; 99MO-JF03929.
 XX
 PR 24-JUL-1998; 98UP-0208820.
 PR 07-AUG-1998; 98UP-0224105.
 PR 25-AUG-1998; 98UP-0238116.
 PR 09-SEP-1998; 98UP-0254736.
 PR 25-SEP-1998; 98UP-0275505.
 XX
 PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.
 XX
 PI Kato S, Kimura T;
 XX
 DR WPI; 2000-182694/16.
 DR P-PSDB; AAY94861.
 XX
 PT Novel human proteins having hydrophobic domains useful for treating
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
 XX multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
 PS Claim 3; Page 217-218; 351bp; English.
 XX
 XX This sequence encodes a human protein of the invention, which has
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a
 CC genetic marker. The protein can also be used as a marker, and to identify
 CC potential genetic disorders. The DNA and protein can also be used as
 CC nutritional sources or supplements. The protein exhibits cytokine, cell
 CC proliferation, cell differentiation activities and induces production of
 CC other cytokines in certain cell populations. The protein also exhibits
 CC immune stimulating or immune suppressing activity. It can be used in the
 CC treatment of various immune deficiencies and disorders, and to treat

CC infectious diseases caused by viral, bacterial, fungal or other
 CC infections. The protein is also used for treating autoimmune disorders
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
 CC arthritis. It is also useful in the treatment of allergic reactions and
 CC conditions such as asthma, and in immune suppression after organ
 CC transplantation. The protein is useful in regulation of haematopoiesis
 CC and consequently in the treatment of myeloid or lymphoid cell
 CC deficiencies. It is also used in compositions for tissue growth or
 CC regeneration. The protein is also used in the treatment of osteoporosis
 CC or osteoarthritis and in the treatment of periodontal disease and other
 CC tooth repair processes. The protein is used in the treatment of nervous
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and
 CC Huntington's disease. The protein is useful for protection or regeneration and
 CC treatment of lung or liver fibrosis, reperfusion injury in various
 CC tissues, and conditions resulting from systemic cytokine damage. They are
 CC also used for promoting or inhibiting tissue differentiation. They are
 CC also used as contraceptives since they exhibit activin or inhibin related
 CC activities and as a fertility inducing therapeutic. They are used for
 CC treating various coagulation disorders and in treatment and prevention of
 CC conditions resulting from coagulation activities e.g. myocardial
 CC infarction or stroke. They also acts as receptors, receptor ligands or
 CC inhibitors or agonists of receptor/ligand interactions. They are used to
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
 CC reperfusion injury, arthritis, and nephritis. They can be used to
 CC prevent tumours.

XX Sequence 297 BP: 81 A; 68 C; 72 G; 76 T; 0 other;

Alignment Scores:

Pred. No.:	1,18e-57	Length:	297
Score:	504.00	Matches:	98
Percent Similarity:	100.00%	Conservative:	1
Best Local Similarity:	98.99%	Mismatches:	0
Query Match:	99.21%	Indels:	0
DB:	21	Gaps:	0

US-09-801-115B-2 (1-99) x AAA15919 (1-297)

QY 1 MetAspAsnValAlaGlnPolysVilLeVehHsArpProhCysPheSerVallyGlyHis 20
 Db 1 ATGATACGTCGCGCGGAAATAAACATCGCCCTTCCTTCATGTGAAAGGCGCAC 60
 QY 21 VallyMetLeuAqLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
 Db 61 GTGAAGATGCTGCGCGCTGATATATCACTCATGTGAAACAGATTCATCTCATC 120
 QY 41 ValSerValLeuAlaLeuIlePProGluThrThrThreuthValGlyGlyValPhe 60
 Db 121 GTATCTGTGTGGCACTGATACAGAAACCAACATTTGACAGTTGGTGGAGGGGTGTT 180
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrrAqVlyLeuLeu 80
 Db 181 GCACCTTGTGACAGAGATATGCTGCTTGCACGCGGGCCCTTATTCCGGACCTCTG 240
 QY 81 PheAsnProSerGlyProTyGlnLysLeuProValHisGluVlySLyGluValIleu 99
 Db 241 TTCAATCCACGGGCTCTTACCAAGAAAGCCCTGTGATGATAAAAGAAAGTTTG 297

RESULT 15

AAA15929 standard; cDNA; 467 BP.

XX AAA15929;

XX 12-JUN-2000 (first entry)

DE Human protein clone HP10357 full length coding sequence.

XX Human protein; hydrophobic domain; nutritional source; haematopoiesis;

KW cytokine production; cell proliferation; cell differentiation;

KW immune deficiency; infectious disease; autoimmune disorder; asthma;

KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;

KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;

KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy; ss.

XX Homo sapiens.

XX MO200005367-A2.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-JP03929.

XX 24-JUL-1998; 98JP-0208820.

XX 07-AUG-1998; 98JP-0224105.

XX 25-AUG-1998; 98JP-0238116.

XX 09-SEP-1998; 98JP-0254736.

XX 29-SEP-1998; 98JP-0275505.

XX (SAGA) SAGAMI CHEM RES CENT.

XX (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI; 2000-182694/16.

XX P-PsDB; AAY94861.

XX Novel human proteins having hydrophobic domains useful for treating

XX osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,

XX multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -

XX Claim 4: Page 228; 35pp; English.

XX This sequence encodes a human protein of the invention, which has

XX hydrophobic domains. The DNA sequences can be used as a probe or as a

XX genetic marker. The protein can also be used as a marker, and to identify

XX potential genetic disorders. The DNA and protein can also be used as

XX nutritional sources or supplements. The protein exhibits cytokine, cell

XX proliferation, cell differentiation activities and induces production of

XX other cytokines in certain cell populations. The protein also exhibits

XX immune stimulating or immune suppressing activity. It can be used in the

XX treatment of various immune deficiencies and disorders, and to treat

XX infectious diseases caused by viral, bacterial, fungal or other

XX infections. The protein is also used for treating autoimmune disorders

XX such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid

XX arthritis. It is also useful in the treatment of allergic reactions and

XX conditions such as asthma, and in immune suppression after organ

XX transplantation. The protein is useful in regulation of haematopoiesis

XX and consequently in the treatment of myeloid or lymphoid cell

XX deficiencies. It is also used in compositions for tissue growth or

XX regeneration. The protein is also used in the treatment of osteoporosis

XX or osteoarthritis and in the treatment of periodontal disease and other

XX tooth repair processes. The protein is used in the treatment of nervous

XX system disorders such as Alzheimer's disease, Parkinson's disease, and

XX Huntington's disease. They are useful for protection or regeneration and

XX treatment of lung or liver fibrosis, reperfusion injury in various

XX tissues, and conditions resulting from systemic cytokine damage. They are

XX also used for promoting or inhibiting tissue differentiation. They are

XX also used as contraceptives since they exhibit activin or inhibin related

XX activities and as a fertility inducing therapeutic. They are used for

XX treating various coagulation disorders and in treatment and prevention of

XX conditions resulting from coagulation activities e.g. myocardial

XX infarction or stroke. They also acts as receptors, receptor ligands or

XX inhibitors or agonists of receptor/ligand interactions. They are used to

XX treat inflammatory conditions such as septic shock, sepsis, ischaemia

XX reperfusion injury, arthritis, and nephritis. They can be used to

XX prevent tumours.

XX Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other;

XX Alignment Scores:

Pred. No.: 2.19e-57 Length: 467
Score: 504.00 Matches: 98
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 98.99% Mismatches: 0
Query Match: 99.21% Indels: 0
DB: 21 Gaps: 0

US-09-801-115B-2 (1-99) x AAA15929 (1-467)

OY 1 MetAspAsnValAlaGlnProLysIleLeuSHisArgProPheCysPheSerValIleGlyHis 20
Db 114 ATGATACGTCGACCGCAAAATATAACATCGCCCTTCTGCTTCAGTGTGAAGGCCAC 173
OY 21 ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 174 GTGAAGATGCTGCGGCTGTGATATTATCACTCAGTACACAGATATCATGCTCATC 233
OY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 234 GTATCTGTGTGGCACTGATACCAAGAAACCAACATTGACAGTGTGTGAGGGGTGTTT 293
OY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
Db 294 GCACCTGTGACAGCAGTATGCTGTTCGACAGGGGCCCTTATTACCGAAGCTTCTG 353
OY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
Db 354 TTCAATCCACAGGCTTACACAGCAAAAGCTGTGATGAAAAAAGAAAGTTTG 410

Search completed: January 31, 2004, 04:20:24
Job time : 249 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 31, 2004, 04:09:48 ; Search time 2058 Seconds
(without alignments)
1169.166 Million cell updates/sec

Title: US-09-801-115B-2
Perfect score: 508
Sequence: 1 MDVQPKIKRPFCEYVKGH.....LFNPSGPYQKPKVHEKKEVL 99

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 1215238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -DEV=xlp
-MODEL=frame+ p2n.model -DB=FASTA
-Q=/cgn2_1/USPTO.spool/p/US09801115/runat.30012004.113848.7035/app_query.fasta.1.263
-DB=FAST -QFMT=FASTAP -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09801115 @CGN 1.1.3549 @runat.30012004.113848.7035 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estc1a.*
2: em_estc1b.*
3: em_estc1c.*
4: em_estc1d.*
5: em_estc1e.*
6: em_estc1f.*
7: em_estc1g.*
8: em_estc1h.*
9: gb_estc1.*
10: gb_estc2.*
11: gb_estc3.*
12: gb_estc4.*
13: gb_estc5.*
14: gb_estc6.*
15: em_estc1.*
16: em_estc2.*
17: em_estc3.*
18: em_estc4.*
19: em_estc5.*
20: em_estc6.*
21: em_estc7.*
22: em_estc8.*
23: em_estc9.*
24: em_estc10.*
25: em_estc11.*
26: em_estc12.*
27: em_estc13.*
28: gb_estc1.*

29: gb_gss2.*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	508	100.0	AA911088	AA911088 OK67601.S
2	508	100.0	AI989739	AI989739 W021010.X
3	508	100.0	AM183193	AM183193 XJ67111.X
4	508	100.0	AA516431	AA516431 NE58A03.S
5	508	100.0	AI989747	AI989747 W021109.X
6	508	100.0	BMS53628	BMS53628 AGENCOURT
7	508	100.0	AI826623	AI826623 W055410.X
8	508	100.0	AI128804	AI128804 Q834B08.S
9	508	100.0	AA455042	AA455042 A04A07.S
10	508	100.0	AA429945	AA429945 ZW67110.S
11	508	100.0	AI078580	AI078580 O237H05.X
12	508	100.0	AI743235	AI743235 W090A02.X
13	508	100.0	BUS64679	BUS64679 AGENCOURT
14	508	100.0	BF109912	BF109912 717103.X
15	508	100.0	BF399486	BF399486 U1-R-CAL-
16	508	100.0	BUS65721	BUS65721 AGENCOURT
17	508	100.0	BX091668	BX091668 BX091668
18	508	100.0	BG705303	BG705303 602687808
19	508	100.0	BUS66499	BUS66499 AGENCOURT
20	508	100.0	BUS59247	BUS59247 AGENCOURT
21	508	100.0	BG031757	BG031757 60229819
22	508	100.0	BUS52309	BUS52309 AGENCOURT
23	508	100.0	CB993661	CB993661 AGENCOURT
24	508	100.0	BK422104	BK422104 BX422104
25	508	100.0	BUS53237	BUS53237 AGENCOURT
26	508	99.4	BM472086	BM472086 AGENCOURT
27	505	99.4	BUS66814	BUS66814 AGENCOURT
28	504	99.2	AA989129	AA989129 O075H10.S
29	504	99.2	BGS59072	BGS59072 602579169
30	504	99.2	BG249994	BG249994 602362062
31	502	98.8	BUI89908	BUI89908 AGENCOURT
32	492	96.9	BX436125	BX436125 BX436125
33	492	96.9	BX046689	BX046689 BX464689
34	491	96.7	BF613984	BF613984 602641513
35	484	95.3	AV759888	AV759888 AV759888
36	480	94.5	AI141284	AI141284 Q852H10.S
37	476.5	93.8	AI265924	AI265924 QX68D08.X
38	475	93.5	BF203359	BF203359 601865968
39	475	93.5	W52820	W52820 ZC55C06.X
40	472	92.9	AA876539	AA876539 O048H08.S
41	471.5	92.8	BQ130559	BQ130559 I188A06.X
42	471.5	92.8	BQ613826	BQ613826 I116A04.X
43	471.5	92.8	AA702011	AA702011 Z170D02.S
44	471.5	92.8	BU077917	BU077917 IM65A04.X
45	471.5	92.8		

ALIGNMENTS

RESULT 1
AA911088/c
LOCUS AA911088 386 bp mRNA linear EST 09-JUN-1998
DEFINITION OK67601.61 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519032.3
ACCESSION AA911088
VERSION AA911088.1 GI:3050378
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
EST.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 386)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/BLNI at:
www.bio.11nl.gov/bdip/image/image.html
Insert Length: 381 Std Error: 0.00
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 79.
Location/Qualifiers
1. .386
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1519032"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/clone_lib="NCI CGAP GC4"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 113 a 87 c 81 g 105 t

ORIGIN

Alignment Scores:
Pred. No.: 2.92e-56 Length: 386
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-801-115B-2 (1-99) x AA911086 (1-386)

QY 1 MetApsanValGlnProlySilelySHiaArgProPhCypheserVallysglyHis 20
Db 357 ATGGATTAACGTGCGCGGAAATAAACATCGCCCTTCTGCTTCACTGGAAAGCCAC 298

QY 21 VallyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 297 GTGAAAGTGTGGCGGTGGATATTATCACTGTAACACAGATTTCATGCTCATC 238

QY 41 ValSerValleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 237 GTATCTGTGTGGCACTGATACCAAGAACCAATTGACAGTTGGAGGGGCTTTT 178

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraGlySLeuLeu 80
Db 177 GCACCTGTGACAGCATATCTGCTTGGCCGACGGGGCCCTTATTTACCGAAGCTTCTG 118

QY 81 PheAsnProSerGlyProTyrglnlyslvsProValHisGluylsGluValleu 99
Db 117 TTCATCCAGCGGTCTTACAGAAAAGCCTGTGATGAAAAAAGAGTTTGG 61

RESULT 2 391 bp mRNA linear EST 27-OCT-1999
LOCUS AI989739/c
DEFINITION wu21e10.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone
IMAGE:2520714 3', mRNA sequence.
ACCESSION AI989739

VERSION AI989739.1 GI:5836620
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 391)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through BLNI; contact the
IMAGE Consortium (info@image.11nl.gov) for further information.
Seq primer: -40up from Gibco.
Location/Qualifiers
1. .391
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2520714"
/tissue_type="colonic mucosa from 3 patients with Crohn's
disease"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares_Dieckgraefe_colon_NHCD"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAACTGGAGCGGCGCCCTTTTCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization. Tissue samples
provided by Dr. Brian Dieckgraefe (Washington University,
dieck@im.wustl.edu); colonic mucosa represents a range of
disease involvement from moderate to severe Crohn's
disease; samples include both perforating (fistulas) and
non-perforating samples. Library constructed by Bento
Soares and M. Fatima Bonaldo. "

BASE COUNT 113 a 90 c 81 g 107 t

ORIGIN

Alignment Scores:
Pred. No.: 2.97e-56 Length: 391
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-801-115B-2 (1-99) x AI989739 (1-391)

QY 1 MetApsanValGlnProlySilelySHiaArgProPhCypheserVallysglyHis 20
Db 358 ATGGATTAACGTGCGCGGAAATAAACATCGCCCTTCTGCTTCACTGGAAAGCCAC 299

QY 21 VallyMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db 298 GTGAAAGTGTGGCGGTGGATATTATCACTGTAACACAGATTTCATGCTCATC 239

QY 41 ValSerValleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db 238 GTATCTGTGTGGCACTGATACCAAGAACCAATTGACAGTTGGAGGGGCTTTT 179

QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraGlySLeuLeu 80
Db 178 GCACCTGTGACAGCATATCTGCTTGGCCGACGGGGCCCTTATTTACCGAAGCTTCTG 119

QY 81 PheAsnProSerGlyProTyrglnlyslvsProValHisGluylsGluValleu 99
Db 118 TTCATCCAGCGGTCTTACAGAAAAGCCTGTGATGAAAAAAGAGTTTGG 62

RESULT 3
AW183193/c 396 bp mRNA linear EST 18-NOV-1999
LOCUS x167f11.x1 Soares NFL T GBC S1 Homo sapiens cDNA clone
DEFINITION IMAGE:2662317 3', mRNA Sequence.
ACCESSION AM183193
VERSION AM183193.1 GI:6451679
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 396)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from G1bco.
Location/Qualifiers
1..396
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2662317"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung BHL19W, testis NHT, and B-cell
NCT-CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729086-731399. Subtraction by Benito
Soares and M. Fatima Bonaldo."
BASE COUNT 115 a 92 c 80 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 3,01e-56 Length: 396
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-801-115b-2 (1-99) x AW183193 (1-396)
QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 359 ATGGATTAACGTGACGCGGAAATTAACATGCCCCCTTCTGCTTCAGTGGAGGCGCAC 300
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 299 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACACAGATTATCATCTCATC 240
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 239 GTACTCTGTGGACGATGATCCAGAAACCAACATTGACGTTGGTGGAGGGGTGTTT 180
QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
DB 179 GCACTTGTGACACGATGCTGCTCTGCCACGGGGCCCTTATTATCCGAAACCTCTG 120
QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
|||||

DB 119 TTCATCCACGCGCTCTTACCAAGAAAAAGCCTGTGTCATGAAAAAAGAGTTTG 63
RESULT 4
AA516431/c 399 bp mRNA linear EST 13-AUG-1997
LOCUS ne58a03.s1 NCI_CGAP_C03 Homo sapiens cDNA clone IMAGE:901516 3',
DEFINITION mRNA sequence.
ACCESSION AA516431
VERSION AA516431.1 GI:2255955
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 399)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Elise Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Benito Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www-bio.llnl.gov/bdrp/image/image.html
Insert Length: 527 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amerham.
Location/Qualifiers
1..399
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:901516"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/clone_lib="NCI CGAP C03"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia). digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library went through one round of
normalization."
BASE COUNT 115 a 94 c 81 g 109 t
ORIGIN
Alignment Scores:
Pred. No.: 3.04e-56 Length: 399
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-801-115b-2 (1-99) x AA516431 (1-399)
QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
DB 357 ATGGATTAACGTGACGCGGAAATTAACATGCCCCCTTCTGCTTCAGTGGAGGCGCAC 238
QY 21 ValLysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 297 GTGAAGATGCTGGCGCTGGATATTATCACTCACTGTAACACAGATTATCATCTCATC 228
QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
DB 237 GTACTCTGTGGACGATGATCCAGAAACCAACATTGACGTTGGTGGAGGGGTGTTT 178
|||||

QY 61 AAlaValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
 Db 177 GCACCTTGACAGCAGTATGCTCTTCCACGCGGCCCTTATTACCGAAGCTTCTG 118
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGlnLysLysValLeu 99
 Db 117 TTCAATCCACGCGCTTACAGAAAAAGCCTGTGATGAAAAAAGAGTTTGG 61
 RESULT 5
 AI989747/c 402 bp mRNA linear EST 27-OCT-1999
 LOCUS W21109.x1 Soares Dieckgraefe.colon_NHCD Homo sapiens cDNA clone
 DEFINITION IMAGE:2520713 3', mRNA sequence.
 ACCESSION AI989747
 VERSION AI989747
 KEYWORDS EST.
 SOURCE AI989747.1 GI:5836628
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 402)
 AUTHORS NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -400P from Gibco.
 FEATURES
 source
 1. 402
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2520713"
 /tissue_type="colonic mucosa from 3 patients with Crohn's
 disease"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="Soares Dieckgraefe.colon_NHCD"
 /note="Organ: colon; Vector: pTV73D-Pac (Pharmacia) with a
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTTACCAATCTGAAGTGGAGCGCGCGCTCTTTTCTTTTCTTTT 3']
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pTV73 vector. Library
 went through one round of normalization. Tissue samples
 provided by Dr. Brian Dieckgraefe (Washington University,
 dieck@wustl.edu); colonic mucosa represents a range of
 disease involvement from moderate to severe Crohn's
 disease; samples include both perforating (fistulas) and
 non-perforating samples. Library constructed by Bento
 Soares and M. Fatima Bonalho.

BASE COUNT 113 a 82 g 117 t
 ORIGIN 90 c

Alignment Scores:
 Pred. No.: 3.07e-56 Length: 402
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AI989747 (1-402)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
 Db 368 ATGGATTAACGGTGCAGCCGAAATAAATACATGCCCCCTTCTCAGTGAAGGCGCAC 309
 QY 21 ValLysMetLeuArgLysAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40

Db 308 GTAAAGATGCTGGCGGTGGATATTATCACTCACTGTGAACAACATATTATCATGCTCATC 249
 QY 41 ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
 Db 248 GTATCTGTGTGGACATGATACAGAAACCAACATTTGACCTGTGTGAGGGGTGTTT 189
 QY 61 AAlaValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeu 80
 Db 188 GCACCTTGACAGCAGTATGCTCTTCCACGCGGCCCTTATTACCGAAGCTTCTG 129
 QY 81 PheAsnProSerGlyProTyrGlnLysLysProValHisGlnLysLysValLeu 99
 Db 128 TTCAATCCACGCGCTTACAGAAAAAGCCTGTGATGAAAAAAGAGTTTGG 72
 RESULT 6
 BM553628 404 bp mRNA linear EST 20-FEB-2002
 LOCUS BM553628
 DEFINITION AGENCOURT_6541772 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5740478
 5', mRNA sequence.
 ACCESSION BM553628
 VERSION BM553628.1 GI:18792524
 KEYWORDS EST.
 SOURCE BM553628.1 GI:18792524
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 404)
 AUTHORS NIH-MGC <http://mhc.ncbi.nlm.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 High quality sequence stop: 403.
 Location/Qualifiers
 1. 404
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5740478"
 /tissue_type="duodenal adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 88"
 /note="Organ: small intestine; Vector: PCMV-SPORT6;
 Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
 oligo-dT primed. Average insert size 1.767 kb. Library
 enriched for full-length clones and constructed by Life
 Technologies. Note: this is a NIH_MGC Library."

BASE COUNT 121 a 80 c 87 g 116 t
 ORIGIN 80 c

Alignment Scores:
 Pred. No.: 3.09e-56 Length: 404
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-801-115B-2 (1-99) x BM553628 (1-404)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
 Db 32 ATGGATTAACGGTGCAGCCGAAATAAATACATGCCCCCTTCTCAGTGAAGGCGCAC 91

QY 21 VallysMetleuArgleuAapllelleasSerleuValThrValPheMetleulle 40
 Db 92 GTAAAGATGCTGGCGCGGATATATTAACCTGATGTAACAACAGATTCATGCTCATC 151
 QY 41 ValSerValleuAlaLeuIleProGluThrThrThrleuThrValGlyGlyValPhe 60
 Db 152 GTATCTGTGTGGACGATACCAAGAAACCAACATTGACATTGGAGGGGCTTTT 211
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeu 80
 Db 212 GCACCTGTGACAGAGATGCTGCTTCCGACGCGGCCCTTATTACCGGAAGCTTCTG 271
 QY 81 PheAsnProSerGlyProTyrgLysLysProValHisGluLysGluValleu 99
 Db 272 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAAAAGAAAGTTTG 328

RESULT 7
 A1826623/c 409 bp mRNA linear EST 21-DEC-1999
 LOCUS W35d10.x1 NCI_CGAP_P122 Homo sapiens cDNA clone IMAGE:2417395 3',
 mRNA sequence.
 A1826623
 ACCESSION A1826623.1 GI:5447294
 VERSION A1826623.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 409)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS NCI-CGAP Consortium
 TITLE Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 www-bio.lnl.gov/bdrrp/image/image.html
 Insert Length: 462 Std Error: 0.00
 Seq primer: -40UP from Gibco.

FEATURES
 source
 1..409
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2417395"
 /sex="male"
 /tissue_type="normal prostate"
 /lab_host="DH10B"
 /clone_idb="NCI CGAP P122"
 /note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
 with a modified polylinker; 1st strand cDNA was prepared
 from normal prostate bulk tissue, and was then primed with
 a Not I - oligo (dT) primer. Double-stranded cDNA was
 ligated to Eco RI adaptors (Pharmacia), digested with Not
 I and cloned into the Not I and Eco RI sites of the
 modified pT73 vector. Library is normalized, and was
 constructed by Bento Soares and M. Fatima Bernaldo."

BASE COUNT 112 a 94 c 80 g 123 t

ORIGIN
 Alignment Scores:
 Pred. No.: 3.14e-56 Length: 409
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatch: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x A1826623 (1-409)

QY 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerValLysGlyHis 20
 Db 367 ATGGATTAAGCTGACGCGGAAATTAACATCGCCCTTCCTGCTGATGGAAGGCAC 308
 QY 21 VallysMetleuArgleuAapllelleasSerleuValThrValPheMetleulle 40
 Db 307 GTAAAGATGCTGGCGCGGATATATTAACCTGATGTAACAACAGATTCATGCTCATC 248
 QY 41 ValSerValleuAlaLeuIleProGluThrThrThrleuThrValGlyGlyValPhe 60
 Db 247 GTATCTGTGTGGACGATACCAAGAAACCAACATTGACATTGGAGGGGCTTTT 188
 QY 61 AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeu 80
 Db 187 GCACCTGTGACAGAGATGCTGCTTCCGACGCGGCCCTTATTACCGGAAGCTTCTG 128
 QY 81 PheAsnProSerGlyProTyrgLysLysProValHisGluLysGluValleu 99
 Db 127 TTCATCCACGCGGTCTTACCAAGAAAGCCTGTGCATGAAAAAGAAAGTTTG 71

RESULT 8
 A1128804/c 423 bp mRNA linear EST 05-OCT-1998
 LOCUS ga94808.s1 Soares fetal heart NBH119W Homo sapiens cDNA clone
 IMAGE:1694391 3', mRNA sequence.
 A1128804
 ACCESSION A1128804.1 GI:3597318
 VERSION A1128804.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 423)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 AUTHORS NCI-CGAP Consortium
 TITLE Tumor Gene Index
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 382 Std Error: 0.00
 Seq primer: -40m13 fwd. RT from Amersham
 High quality sequence stop: 413.

FEATURES
 source
 1..423
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1694391"
 /sex="unknown"
 /dev_stage="19 weeks"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_idb="Soares fetal heart NBH119W"
 /note="Organ: heart; Vector: pT73D (Pharmacia) with a
 modified polylinker; Site: 1: Not I; Site 2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo (dT) primer [5'
 TGTTACCAATCTAGAGTGGAGCGCGCATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 TGTTACCAATCTAGAGTGGAGCGCGCATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
 double-stranded cDNA was size selected, ligated to Eco RI
 adaptors (Pharmacia), digested with Not I and cloned into
 the Not I and Eco RI sites of a modified pT73 vector
 (Pharmacia). Library went through one round of
 normalization to a Cot = 5. Library constructed by
 M. Fatima Bernaldo. This library was constructed from the
 same fetus as the fetal lung library, Soares fetal lung
 NBH119W."

BASE COUNT 116 a 101 c 89 g 117 t

ORIGIN
 Alignment Scores:

Pred. No.: 3,27e-56 Length: 423
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x A1128804 (1-423)

Qy 1 MetaspasVAlGInProLySileYSH:ARgProPhCySPheSeValLySGlyHis 20
 Db 353 ATGATTAACGTGCAGCCGAAATAAATCAATCGCCCTTCTGCTTCACTGTAAGGCCAC 294
 Qy 21 VallysMetLeuAryLeuAspIleIleAsnSerLeuValThrThyValPheMetLeuIle 40
 Db 293 GTGAAGATGCTGGCGCTGATATTAATCACTGTAACAGTATTCATGCTATC 234
 Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThreuthrValGlyGlyValPhe 60
 Db 233 GTATCTGTGTGGCAGTATACCAAGAACCAACATGACATGAGTGTGAGGGGTCTT 174
 Qy 61 AlaleuValThrAlaValCySyleuAlaAspGlyAlaLeuIleTyArgLyLeu 80
 Db 173 GCACCTTGACAGCAGTATGCTCTTCCGACGGGCGCTTATTATTCAGGAGCTTCTG 114
 Qy 81 PheAsnProSerGlyProTyGlnLySylsProValHisGluLySylsGluValLeu 99
 Db 113 TTCATCCGACGGTCTTACCAAAAAGCTGTGATGATAAAAAGAAAGTTTG 57

RESULT 9
 AA455042/c 427 bp mRNA linear EST 06-JUN-1997
 LOCUS aa04a07.81 Soares_NHMPu_51 Homo sapiens cDNA clone IMAGE:812244
 DEFINITION 3', mRNA sequence.
 ACCESSION AA455042
 VERSION AA455042.1 GI:2177818
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 427)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997

TITLE
 JOURNAL
 COMMENT Unpublished
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -41m3 fwd. ET from Amersham
 High quality sequence stop: 395.

FEATURES

source
 1. .427
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="GDB:6043155"
 /db_xref="taxon:9606"
 /clone="IMAGE:812244"
 /cissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /clone_lib="Soares NHMPu_51"
 /note="Organ: mixed (see below); Vector: pTT73D-Pac
 (Pharmacia) with a modified polylinker; Site 1: Not I;
 Site 2: Eco RI; Equal amounts of plasmid DNA from three
 normalized libraries (melanocyte 2NBH, pregnant uterus

NbHPu, and fetal heart NbH19w) were mixed, and as circles
 were made in vitro. Following HAP purification, this DNA
 was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from pools of
 5,000 clones made from the same 3 libraries. The pools
 consisted of I.M.A.G.E. clones 260232-265223,
 340488-345479, and 484488-489479."

BASE COUNT 119 a 101 c 91 g 116 t
 ORIGIN

Alignment Scores:
 Pred. No.: 3,31e-56 Length: 427
 Score: 508.00 Matches: 99
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 9 Gaps: 0

US-09-801-115B-2 (1-99) x AA455042 (1-427)

Qy 1 MetaspasVAlGInProLySileYSH:ARgProPhCySPheSeValLySGlyHis 20
 Db 356 ATGATTAACGTGCAGCCGAAATAAATCAATCGCCCTTCTGCTTCACTGTAAGGCCAC 297
 Qy 21 VallysMetLeuAryLeuAspIleIleAsnSerLeuValThrThyValPheMetLeuIle 40
 Db 296 GTGAAGATGCTGGCGCTGATATTAATCACTGTAACAGTATTCATGCTATC 237
 Qy 41 ValSerValLeuAlaLeuIleProGluThrThrThreuthrValGlyGlyValPhe 60
 Db 236 GTATCTGTGTGGCAGTATACCAAGAACCAACATGACATGAGTGTGAGGGGTCTT 177
 Qy 61 AlaleuValThrAlaValCySyleuAlaAspGlyAlaLeuIleTyArgLyLeu 80
 Db 176 GCACCTTGACAGCAGTATGCTCTTCCGACGGGCGCTTATTATTCAGGAGCTTCTG 117
 Qy 81 PheAsnProSerGlyProTyGlnLySylsProValHisGluLySylsGluValLeu 99
 Db 116 TTCATCCGACGGTCTTACCAAAAAGCTGTGATGATAAAAAGAAAGTTTG 60

RESULT 10
 AA429945/c 432 bp mRNA linear EST 16-OCT-1997
 LOCUS zw67f10.81 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:781291
 DEFINITION 3', mRNA sequence.
 ACCESSION AA429945
 VERSION AA429945.1 GI:2113244
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wyllie,
 T., Waterston, R., and Wilson, R.
 WashU-Merck EST Project 1997

TITLE
 JOURNAL
 COMMENT Unpublished
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -41m3 fwd. ET from Amersham
 High quality sequence stop: 421.

FEATURES

source
 1. .432
 /organism="Homo sapiens"
 /mol_type="mRNA"

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/db_xref="taxon:9606"
/clone="IMAGE:781291"
/sex="male"
/lab host="DH10B"
/clone_lib="Soares testis NHT"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAGAGGAGCGCCGCAATTTTATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. Library
went through one round of normalization to Cots, and was
constructed by Bento Soares and M. Fatima Bonaldo. "
```

BASE COUNT 119 a 101 c 92 g 120 t

ORIGIN

Alignment Scores:

Pred. No.:	3,36e-56	Length:	432
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9	Indels:	0
DB:		Gaps:	0

US-09-801-115B-2 (1-99) x AA429945 (1-432)

QY 1 MetaspasmyValGlnProlystleYSHisArgProPheCySpheSerVallySGlyHis 20

DB 361 ATGGATACGCGCGAGGAAATAAACATCGCCCTTCTGCTTCAAGTGAAGGCGCAC 302

QY 21 VallySerMetLeuArgLeuAspIlelleasSerLeuValThrThrValPheMetLeuIle 40

DB 301 GTGAGAGTCTGCGCGCTGGATTTATTCACACTGTAACACAGATTCATCTCATC 242

QY 41 ValSerValleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

DB 241 GTATCTGTGTGGCAGTACGATACAGAAACCAACATTCAGTGGAGGGGCTTT 182

QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraArgVlsLeuLeu 80

DB 181 GCATCTGTGACAGAGATGCTGCTTCCGACGCGGCGCTTATTTACCGAACCTTCTG 122

QY 81 PheAsnProSerGlyProTyrglnlyslYsProValHisGluIlyslYsGluValLeu 99

DB 121 TTCATCCACGCGGCTCTTACCAAGAAAGCCTGTGATGAAAAAGAGTTTGG 65

RESULT 11

LOCUS A1078580 452 bp mRNA linear EST 10-AUG-1998

DEFINITION 3', mRNA sequence.

ACCESSION A1078580

VERSION A1078580.1 GI:3412988

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Seq primer: -40ml3 fwd: ET from Amersham High quality sequence stop: 410. Location/Qualifiers

FEATURES

source 1..452

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1677561"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab host="DH10B"
/clone_lib="Soares_NhMPu_S1"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NBHM, pregnant uterus
NBHPU, and fetal heart NBH15W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
```

BASE COUNT 125 a 110 c 97 g 120 t

ORIGIN

Alignment Scores:

Pred. No.:	3,56e-56	Length:	452
Score:	508.00	Matches:	99
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	9	Indels:	0
DB:		Gaps:	0

US-09-801-115B-2 (1-99) x A1078580 (1-452)

QY 1 MetaspasmyValGlnProlystleYSHisArgProPheCySpheSerVallySGlyHis 20

DB 359 ATGGATACGCGCGAGGAAATAAACATCGCCCTTCTGCTTCAAGTGAAGGCGCAC 300

QY 21 VallySerMetLeuArgLeuAspIlelleasSerLeuValThrThrValPheMetLeuIle 40

DB 299 GTGAGAGTCTGCGCGCTGGATTTATTCACACTGTAACACAGATTCATCTCATC 240

QY 41 ValSerValleuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60

DB 239 GTATCTGTGTGGCAGTACGATACAGAAACCAACATTCAGTGGAGGGGCTTT 180

QY 61 AlaleuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyraArgVlsLeuLeu 80

DB 179 GCATCTGTGACAGAGATGCTGCTTCCGACGCGGCGCTTATTTACCGAACCTTCTG 120

QY 81 PheAsnProSerGlyProTyrglnlyslYsProValHisGluIlyslYsGluValLeu 99

DB 119 TTCATCCACGCGGCTCTTACCAAGAAAGCCTGTGATGAAAAAGAGTTTGG 63

RESULT 12

LOCUS A1743235 453 bp mRNA linear EST 20-DEC-1999

DEFINITION W90A02.x1 Soares NSF P8.9W OT PA_P.S1 Homo sapiens cDNA clone IMAGE:2372330 3', mRNA sequence.

ACCESSION A1743235

VERSION A1743235.1 GI:5111523

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.

LOCUS BF109912 468 bp mRNA linear EST 20-OCT-2000
DEFINITION 7171F03.x1 Soares NSF_F8_9W_OT_PA_P.S1 Homo sapiens cDNA clone
IMAGE:3526805.3' similar to TR:09UI41 09UI41 CHEMOKINE-LIKE FACTOR
1. [1] ;, mRNA sequence.
ACCESSION BF109912
VERSION BF109912.1 GI:10939602
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 468)
AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-f@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Seq primer: -40UP from Gibco.
FEATURES
source
1..468
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3526805"
/lab_host="DH10B"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P.S1"
/note="Organ: pooled; Vector: pT73D-Pac (pharmacia) with
a modified polylinker; Site 1: Not I; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
30984-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HP-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 127 a 116 c 102 g 123 t
ORIGIN
Alignment Scores:
Pred. No.: 3,72e-56 Length: 468
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x BF109912 (1-468)

QY 1 MetAspAsnValGlnProlysilElySHsArgProPhCySpheSerVallySGlyHis 20
DB 362 ATGGATTAACGTGACGCCGAAATMAACATCGCCCTTCCTGCTGCACTGGAAGGCCAC 303

QY 21 VallysmetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
DB 302 GTGAAGATGCTGGCGGCTGATATTATCACTGATGAACACAGATTATCATGCTATC 243

QY 41 ValSerValLeuValaleuIleProGluThrThrThrLeuThrValGlyGlyValAlphe 60
DB 242 GTATCTGTGTGGACATGATACCAAGAACCAACATTTGACATGATGATGAGGGGCTTTT 183

QY 61 AlaleuValThrAlaValAlCySLeuAlaAspGlyAlaLeuIleYrArgVLSLeuLeu 80
DB 182 GCACCTGTGACAGCATGATGCTGCTTCCGACGGGGCCCTTATTATCCGGAAGCTTCTG 123

QY 81 PheAsnProSerGlyProTyrglnlyLysProValHisGlyLysGlyValIleu 99
DB 122 TTCATATCCACGAGCGTCTTACCAAGAAAGCCGTGTCATGAAAAAGAGAGTTTG 66

RESULT 15
LOCUS BF399486/c
DEFINITION UI-R-CA1-bjb-b-12-0-UI.s1 UI-R-CA1 Rattus norvegicus cDNA clone
UI-R-CA1-bjb-b-12-0-UI 3', mRNA sequence.
ACCESSION BF399486
VERSION BF399486.1 GI:11384494
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 510)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@iowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLVA=Yes.
FEATURES
source
1..510
Location/Qualifiers
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CA1-bjb-b-12-0-UI"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; The UI-R-CA1
library is a subtracted library derived from the following
tissues: thalamus, cerebellum, hypothalamus, medulla, pons
'midbrain, cerebral cortex, corpus striatum, testis, and
hippocampus. For a detailed description of the library
from which this clone was derived, please visit our web
site at ratseq.eng.uiowa.edu. The subtraction has been
previously described in (Bonaldo, Lennon and Soares,
Genome Research 6:791-806, 1996)
TAG_SEQ=None found"

BASE COUNT 130 a 131 c 104 g 145 t
ORIGIN
Alignment Scores:
Pred. No.: 4.14e-56 Length: 510
Score: 508.00 Matches: 99
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-801-115B-2 (1-99) x BF399486 (1-510)

QY 1 MetAspAsnValGlnProlysilElySHsArgProPhCySpheSerVallySGlyHis 20

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Db      371  ATGGATAACGTCAGCCGAAATAAATACATGCCCCCTTCTGCTTCAGTGTGAAAGGCCAC 312
Qy      21   ValIysMetLeuArgLeuAspIleIleAsnSerLeuValThrThrValPheMetLeuIle 40
Db      311  GTGAAGATGCTGCGGCTGGATATTATCACTACACTGCTGTAACACAGTATTCAATGCTCATC 252
Qy      41   ValSerValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyValPhe 60
Db      251  GTATCTGTGTGGACACTGATCCAGAAACCAACATTGACAGTTGGTGGAGGGGTGTTT 192
Qy      61   AlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeu 80
Db      191  GCACTGTGACAGCAGATATGCTGCTTGCCGACGCGGCCCTTATTATACCGGAAGCTTCTG 132
Qy      81   PheAsnProSerGlyProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
Db      131  TTCATCCCGCGGTCCTTACCAGAAAAAGCCTGTGCAAGAAAAAAGAAAGTTTGG 75

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Search completed: January 31, 2004, 05:25:28
 Job time : 2061 secs